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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>5/30/03</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>6/4/03</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>20</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>K</u>	Other _____	Other (specify) _____

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NOT AVAILABLE

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:38:24 ; Search time 1828.75 Seconds
(without alignments)
11219.411 Million cell updates/sec

Title: US-09-576-424-1

Perfect score: 705

Sequence: 1 atgagggtcccgctcagct.....ccctacagaatgttcatga 705

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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GenEmbl:*

1: gb_ba:*

2: gb_hgt:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sta:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mui:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sta:*

28: em_un:*

29: em_vi:*

30: em_hgt_hum:*

31: em_hgt_inv:*

32: em_hgt_other:*

33: em_hgt_mus:*

34: em_hgt_pln:*

35: em_hgt_rod:*

36: em_hgt_mam:*

37: em_hgt_vrt:*

38: em_sy:*

39: em_hgt_hum:*

40: em_hgt_mus:*

41: em_hgt_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	705	100.0	705	6	AR108862	AR108862 Sequence
2	585.2	83.0	702	6	AR135374	AR135374 Sequence
3	574.4	81.5	820	9	AB064177	AB064177 Homo sapi
4	571.2	81.0	901	9	BC028090	BC028090 Homo sapi
5	569.8	80.8	803	9	HSIGVL022	HSIGVL022 Human rearr
6	561.8	79.7	747	9	HSIGVL031	HSIGVL031 Human rearr
7	542.8	77.0	648	9	HSAG30319	HSAG30319 Homo sapi
8	540.2	76.6	711	6	AR108866	AR108866 Sequence
9	538	76.3	790	9	AB064230	AB064230 Homo sapi
10	534.4	75.8	826	9	AB064174	AB064174 Homo sapi
11	529.6	75.1	824	9	AB064176	AB064176 Homo sapi
12	526.4	74.7	813	9	AB064167	AB064167 Homo sapi
13	525.2	74.5	895	9	BC022823	BC022823 Homo sapi
14	524	74.3	725	9	HSIGVL002	HSIGVL002 Human rearr
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16	522	74.0	788	9	AB064168	AB064168 Homo sapi
17	520.8	73.9	904	6	AX402510	AX402510 Sequence
18	517	73.3	1154	9	BC007782	BC007782 Homo sapi
19	516.8	73.3	821	9	AB064179	AB064179 Homo sapi
20	516	73.2	791	9	HSIGVL028	HSIGVL028 Human rearr
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23	512	72.6	872	6	E01593	E01593 cDNA encodi
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31	507.2	71.9	794	9	AB064214	AB064214 Homo sapi
32	507.2	71.9	807	9	AB064165	AB064165 Homo sapi
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36	499	70.8	788	9	AB064211	AB064211 Homo sapi
37	497.6	70.6	796	9	AB064182	AB064182 Homo sapi
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ALIGNMENTS

RESULT 1
AR108862
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR108862
Sequence 1 from patent US 6113898.
AR108862
AR108862.1 GI:12825138
Unknown.
Unclassified.
1 (bases 1 to 705)
Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.
Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
Patent: US 6113898-A 1 05-SEP-2000;

705 bp
DNA
linear
PAT 14-FEB-2001

Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics

JOURNAL

Unpublished
2 (bases 1 to 820)

REFERENCE

Kurosawa,Y.
Direct Submission

TITLE

Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyooka 470-1192, Japan

JOURNAL

(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)

Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.

Location/Qualifiers

1. .820

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="L37"

/notes="mixture of tissues:tonsils, umbilical cords,
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1. .>820

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/genes="IGL"

/note="pelB signal peptide"

183 a 240 c 238 g 159 t

BASE COUNT

ORIGIN

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Best Local Similarity

Matches 599; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Score 574.4; DB 9; Length 820;

Pred. No. 2.9e-130;

Query Match

Best Local Similarity

Matches 599; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Score 574.4; DB 9; Length 820;

Pred. No. 2.9e-130;

Query Match

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Pred. No. 2.9e-130;

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542 TGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCACAGCTACTCTGA 601

548 TGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCACAGCTACTCTGA 607

602 GCTGACGCTGAGCAGTGGAAAGTCCACAGAAAGTACAGCTGCCAGGTACGCGCAAG 661

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668 GGAGCACCCTGGAGAGACAGTGGCCCTTACAGAAATGTTTC 707

BC028090 901 bp mRNA linear PRI 01-MAY-2002

Homo sapiens, clone MGC:40381 IMAGE:4184029, mRNA, complete cds.

BC028090

BC028090.1 GI:20380867

MGC.

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 901)

Strausberg,R.

Direct Submission

Submitted (08-APR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc.mgc@nih.gov

Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L.,

Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,

Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tourgeon,C.,

Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,

Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: IRAC Plate: 62 Row: k Column: 16

This clone was selected for full length sequencing because it

passed the following selection criteria: Similarity but not

identity to protein.

Location/Qualifiers

1. .901

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/db_xref="taxon:9606"

/clone="MGC:40381 IMAGE:4184029"

/tissue type="Brain, glioblastoma with EGFR amplification"

/clone_lib="NCI CGAP_Brn64"

/lab host="DH10B"

/note="Vector: pCMV-SPORT6"

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/codon_start=1

FEATURES

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="MGC:40381 IMAGE:4184029"

/tissue type="Brain, glioblastoma with EGFR amplification"

/clone_lib="NCI CGAP_Brn64"

/lab host="DH10B"

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CDS

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Best Local Similarity 90.8%; Pred. No. 1.9e-129;
Matches 632; Conservative 0; Mismatches 58; Indels 6; Gaps 2;
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DB 50 CCGTCTCTCTCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 106
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DB 107 TGACTCAGCACCTCGGTCTCAGTGTCCAGGACAGACGGCCAGGATCACCTGTGGG 166
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QY 608 CGCTGAGCAGTGAAGTCCCAAGAGTACAGTGTCCAGGTTCAGCATGAAGGAGCA 667
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QY 668 CCGTGGAGAGACAGTGGCCCTACAGATGTTTCAAT 703
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DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57812
VERSION X57812.1 GI:33723
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 803)

Direct Submission

Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

2 (bases 347 to 393)

Combiato.G. and Klobeck,H.G.

V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism

Eur. J. Immunol. 21 (6), 1513-1522 (1991)

91257162

1904362

for overlapping sequences see: X51754-55; J00252-54; M15641-42.

Location/Qualifiers

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/note="CDNA"

/evidence=experimental

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misc_feature 67..391

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Best Local Similarity 92.8%; Pred. No. 3.9e-129;

Matches 596; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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DB 68 CCTATGTGCTGACTCAGCCACCTCGGTGTCTAGTGTCCCGAGGAGCGGCGGATTA 127

QY 122 CCTGTGGGGGACACACAGTAGAATATATGTCCATGTTTACAGCAGAGCCAGCGC 181

DB 128 CCTGTGGGGGAAATCAACATTGCAAGTAAAGTGTCTGCTACCGAGCAGAGCCAGGCC 187

QY 182 GGGCCCCCTATCTGTCTATGATGATGACGCGGCCCTCAGGGATCCCTGAGCGAT 241

DB 188 AGGCCCCCTGTGTGTCTATGATGATGACGCGGCCCTCAGGGATCCCTGAGCGAT 247


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QY 242 TCTCTGGCTCCAAATCAGGGAAACACGCCACCTGACCATCAACGGGTGCGAGCGGGG 301
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Db 368 GAGGGACCAAGCTGACCGTCTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 427
QY 422 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCTGAGGCTGAGTGTCTCATAGTACT 481
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QY 482 TCTACCGGGGAGCGGTGACAGTGGCTGGAAGGACAGATAGCAGCCCGTCAAGCGGGAG 541
Db 488 TCTACCGGGGAGCGGTGACAGTGGCTGGAAGGACAGATAGCAGCCCGTCAAGCGGGAG 547
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Db 548 TGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACGGCGGACAGCTACTCTGA 607
QY 602 GCTGTAGCGCTGAGAGTGAAGTCCCAAGAGCTACAGTCCAGGTCCAGCATGAAG 661
Db 608 GCCTGAGCGCTGAGAGTGAAGTCCCAAGAGCTACAGTCCAGGTCCAGCATGAAG 667
QY 662 GGAGACCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703
Db 668 GGAGACCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 709
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RESULT 6

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LOCUS Human rearranged immunoglobulin lambda light chain mRNA.
DEFINITION X57821
ACCESSION X57821
VERSION 1
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Klobeck, H.G.
Direct Submission
Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
2 (bases 340 to 386)
Combratio, G. and Klobeck, H.G.
Immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
Eur. J. Immunol. 21 (6), 1513-1522 (1991)
91257162
1904362
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.
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 ACCESSION AB064230
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
 TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 790)
 AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyokake 470-1192, Japan
 (E-mail:kurosawa@fujita-hu.ac.jp, Tel.81-562-93-9387)
 COMMENT Please visit our web site
 URL:http://www.fujita-hu.ac.jp/immunity/
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 ACCESSION AB064174
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 REFERENCE
 AUTHORS
 1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,

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Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyooka 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.

FEATURES
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Matches 569; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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DEFINITION				Homo sapiens IGI mRNA for immunoglobulin lambda light chain VLJ
ACCESSION				AB064167
VERSION				AB064167.1
KEYWORDS				GI:21669540
SOURCE				Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L27.
ORGANISM				Homo sapiens
REFERENCE				1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS				Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
TITLE				Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL				Unpublished
REFERENCE				2 (bases 1 to 813)
AUTHORS				Kurosawa, Y.
TITLE				Direct Submission
JOURNAL				Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for

Db 608 GCCTGACGCTGAGCTGGAAGTCCACAGAGAGCTACAGCTGCCAGGTACGCATGAAG 667
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DEFINITION BC022823
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 KEYWORDS MGC.

SOURCE Homo sapiens.
 ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Strausberg, R.
 TITLE Direct Submission

JOURNAL Submitted (04-FEB-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk

Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: Louis Staudt

cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Martin Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Strott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 42 Row: g Column: 21
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, Genomescan gene prediction, Similarity but not identity
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 Matches 569; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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RESULT 14
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 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 725)
 Klobbeck, H.G.
 DIRECT SUBMISSION

TITLE Submitted (31-JAN-1991) H.G. Klobbeck, Inst fuer Physiologische
 JOURNAL Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
 Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

REFERENCE 2 (bases 355 to 401)
 AUTHORS Combratio, G. and Klobbeck, H.G.
 TITLE V lambda and J lambda-C lambda gene segments of the human
 immunoglobulin lambda light chain locus are separated by 14 kb and
 rearrange by a deletion mechanism

JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
 MEDLINE 91257162

PUBMED 1904362
 COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.
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 Matches 576; Conservative 0; Mismatches 60; Indels 6; Gaps 1;
 QY 62 CCTATGAATGACTCAGCCACCTCGTGTCTAGTGTCCCGAGACAGAGCGCCAGGATCA 121
 DB 82 CCTATGAGTGTACTAGCCACCTCTAGTGTCCCGAGACAGAGCGCCAGGATCA 141
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 DB 142 CTGTCTCTGGATACATATGGGGGATAATATGTCTGTGTATCAGCAGAGCCAGGCC 201
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 DB 202 ACTCCCTGTGTGGTTCATCTTCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGAT 261
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 QY 302 ATGAGCTCACTATTACTGTCTAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
 DB 322 ATGAGGCTCACTATTACTGTCTAGGCGTGGGACAGCAGCACTG-----CGGTATTCGGCG 375
 QY 362 GAGGACCGGGTGAACCTCTAGTTCAGCCCAAGGCTGCCCTCGGTCTCTCTGTTCC 421
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 DB 616 GCCTGACGCTGAGCAGTGGAAAGTCCCAAGAGCTTACAGCTGCCAGGTGACGATGAAG 675
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 VERSION BC032452.1 GI:21595391
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 890)
 Strausberg,R.
 Direct Submission
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgi.nci.nih.gov
 Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc.mgc@nih.gov
 Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
 Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
 Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
 Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
 Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
 McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
 Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,L.-H. and Green,E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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 This clone was selected for full length sequencing because it
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 prediction.
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 26. .727
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:15:24 ; Search time 961.424 Seconds
(without alignments)
11875.950 Million cell updates/sec

Title: US-09-576-424-1

Perfect score: 705

Sequence: 1 atgagggtccgcgcagct.....ccctacagaatgttcataga 705

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits.satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	558.8	79.3	952	14	BQ711447
2	555.6	78.8	931	14	BQ709526
3	555.2	78.8	931	14	BQ711683
4	552	78.3	796	12	BG757730
5	552	78.3	969	14	BQ707953
6	551.2	78.2	921	14	BQ708246

7	548.8	77.8	920	14	BQ711280	BQ712280	AGENCOURT
8	547.2	77.6	925	14	BQ710672	BQ710672	AGENCOURT
9	546	77.4	832	12	BG746204	BG746204	AGENCOURT
10	545.8	77.4	908	14	BQ884067	BQ884067	AGENCOURT
11	545.6	77.4	754	13	B1907909	B1907909	AGENCOURT
12	545.2	77.3	924	12	BG756256	BG756256	AGENCOURT
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14	544.4	77.2	917	14	BQ711587	BQ711587	AGENCOURT
15	542.4	76.9	949	14	BQ709509	BQ709509	AGENCOURT
16	541.6	76.8	1018	14	BM914338	BM914338	AGENCOURT
17	540.8	76.7	947	14	BQ709579	BQ709579	AGENCOURT
18	540.4	76.7	789	13	B1765865	B1765865	AGENCOURT
19	537	76.2	742	13	B1906298	B1906298	AGENCOURT
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21	531	75.3	837	12	BG754193	BG754193	AGENCOURT
22	530.2	75.2	731	10	AV649126	AV649126	AGENCOURT
23	529	75.0	803	12	BG758687	BG758687	AGENCOURT
24	528	74.9	862	12	BF338816	BF338816	AGENCOURT
25	527.4	74.8	942	12	BG686249	BG686249	AGENCOURT
26	525.6	74.6	788	13	BM007725	BM007725	AGENCOURT
27	525	74.5	1010	14	BM914307	BM914307	AGENCOURT
28	520.8	73.9	913	12	BG745387	BG745387	AGENCOURT
29	520.2	73.8	871	12	BG398521	BG398521	AGENCOURT
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32	515.2	73.1	926	13	B1911261	B1911261	AGENCOURT
33	513.8	72.9	868	12	BG745881	BG745881	AGENCOURT
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35	512.6	72.7	864	12	BG756128	BG756128	AGENCOURT
36	508.4	72.1	782	13	BM007795	BM007795	AGENCOURT
37	508.2	72.1	801	13	BM007626	BM007626	AGENCOURT
38	508	72.1	829	12	BG754011	BG754011	AGENCOURT
39	501.8	71.2	688	12	BG745481	BG745481	AGENCOURT
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ALIGNMENTS

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LOCUS BQ711447 952 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8353624 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279618
5', mRNA sequence.
ACCESSION BQ711447
VERSION BQ711447.1 GI:21850346
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 952)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2469 row: h column: 19
High quality sequence stop: 584.
Location/Qualifiers
1. .952


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/clone="IMAGE:4854921"
/clone lib="NIH MGC 48"
/tissue type="primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 177 a 244 c 231 g 143 t 1 others
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Query Match 78.3%; Score 552; DB 12; Length 796;
Best Local Similarity 92.1%; Pred. No. 2.5e-132;
Matches 591; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

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DB 87 CCTATGTGTACTCAGCCACCTCGGTGTCAGTGTCCCGGACAGACGCGCCAGGATTA 146
QY 122 CCTGTGGGGAGACAACAGTAGAATCAATATGTCCACTGGTACACGAGCAAGCCAGCGC 181
DB 147 CCTGTGGGGAAATAACATTGAAGTAAACATGTGCACCTGGTATCAGCAGAGCCAGGCC 206
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QY 542 TGGAGACCAACACCTCCAAACAAAGCAACAAAGTACGCGGCGAGGACTACTGA 601
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RESULT 5
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LOCUS
DEFINITION BQ707953 969 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8353606 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279593
5', mRNA sequence.
ACCESSION BQ707953
VERSION BQ707953.1 GI:21846852
KEYWORDS EST.

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SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 969)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2469 row: g column: 18

High quality sequence stop: 541.

Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"

/db_xref="taxon:9606"

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/lab host="NIH MGC 113"

/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dr priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH MGC Library."

226 a 309 c 251 g 174 t 9 others

BASE COUNT

ORIGIN

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Query Match 78.3%; Score 552; DB 14; Length 969;
Best Local Similarity 89.1%; Pred. No. 2.6e-132;
Matches 620; Conservative 0; Mismatches 70; Indels 6; Gaps 2;

QY 11 CGCTCAGCTCTCTGGGGCTCTCTGCTCTGCTCTCCAGTGCACAGATGCTCTATGAAC 70
DB 28 CGGTCTCTCTCTCGGCTCTCTCTCACTG---CACAGGCTCTGTGACCTCTATGTCC 84
QY 71 TGACTCAGCCACCTCGGTGTCAGTGTCCCGGACAGACGCGGAGTACCTGTGGGG 130
DB 85 TGACTCAGCCACCTCGGTGTCAGTGTGCGGCCCCAGGACAGCGCCAGTATTCTGTGGG 144
QY 131 GAGACAAACAGTAGAATGAATATGTCCTGCTGCTACGAGCAAGCCAGCGCGGCCCTTA 190
DB 145 GAAACACCACTCAAGTAAAGTGTGCTGCTGCTACGAGCAAGCCAGCGCGGCCCTG 204
QY 191 TACTGCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
DB 205 TCTGCTGCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 264
QY 251 CCAAAATCAGGGAACCCGCCCTGACCATCAACGGGTCGAGCCGGGGATGAGGCTG 310
DB 265 CCAATTCGGGAACACGGCCACCTGACCATCATAGTGGGTGAAGCGGGATGAGGCCG 324
QY 311 ACTATTACTGTCTAGGTGTGGGACAGGGCTAGTGATC---ATCCGGTCTTCGGAGGAGGA 367
DB 325 ACTATTACTGTCTAGGTGTGGGATGATGATGATGATGATGATGATGATGATGATGATG 384
QY 368 CCGGGGTGACCGTCTCTAGGTGACCGGCTGCGGCTCTGCTGCTGCTGCTGCTGCTGCTG 427
DB 385 CCAAGTGAACCGTCTCTAGGTGACCGGCTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTG 444
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DB 445 CTTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGCTCTCAAGTGAATCTTCTACC 504

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ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT	216 a	281 c	246 g	176 t	1 others
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Best Local Similarity	88.8%; Pred. No. 1.8e-131;				
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QY	131	GAGACACAGTAAATGATATGCTCCAGTGTACGACGAGCCAGCGCGGCCCTA	190		
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QY	191	TACTGTCTATCTATGATGATGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCT	250		
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 BQ710672
 VERSION
 BQ710672.1
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 925)
 NIH-MGC http://mhc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM2516 row: e column: 10
 High quality sequence stop: 661.
 Location/Qualifiers
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 /lab_host="DH10B (phage-resistant)"
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BASE COUNT 214 a 293 c 239 g 170 t 9 others
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 Query Match 77.6%; Score 547.2; DB 14; Length 925;
 Best Local Similarity 88.6%; Pred. No. 4.6e-131;
 Matches 617; Conservative 0; Mismatches 73; Indels 6; Gaps 2;
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 QY 131 GAGACACAGTAAATGATATGCTCACTGTGTACGACGAGCCAGCGCGGCCCTA 190
 Db 155 GAAACAATATTGGAAGTAGAAGTGTGCACTGTGTACGACGAGACTTCAGGCCAGGCCCTG 214
 QY 191 TACTGTCTATCTATGATGATGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCT 250
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 QY 251 CCAAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTTCGAGCGCGGGATGAGGCTG 310
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 QY 368 CCGGGTGTAGCTCTCTAGGTGACCGCCAGGCTGCCCTCGGTCACTCTGTTCCCGCCCT 427
 Db 395 CCAAGTGTAGCTCTCTAGTGTAGCCAGCCAGGCTGCCCTCGGTCACTCTGTTCCCGCCCT 454
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Db 515 CGGAGCCGTGACAGTGGCTGGAAGCGCAGATAGACCCCGTCAAGCGGGAGTGGAGA 574
QY 548 CCACCAACCCCTCCAAACAAAGCAACAAAGTACCGCGCCAGCAGCTACCTGAGCCTGA 607
Db 575 CCACCAACCCCTCCAAACAAAGCAACAAAGTACCGCGCCAGCAGCTATCTGAGCCTGA 634
QY 608 CCCTGAGCAGTGGAGTCCACAGAGCTCCAGAGCTACAGCTGCCAGTCAAGGAGGCA 667
Db 635 CGCTGAGCAGTGGAGTCCACAGAGCTCCAGAGCTGCCAGTCAAGGAGGCA 694
QY 668 CCCTGAGAGAGCAGTGGCCCTTACAGAAATGTTTCAT 703
Db 695 CCCTGAGAGAGCAGTGGCCCTTACAGAAATGTTTCAT 730

RESULT 9
BG746204/c
LOCUS
DEFINITION
602723726T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4849878 3',
mRNA sequence.
ACCESSION
BG746204
VERSION
BG746204.1 GI:14056857
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 832)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1690 row: d column: 07
High quality sequence stop: 827.
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1..832
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/db_xref="taxon:9606"
/clone="IMAGE:4849878"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 152 a 232 c 263 g 185 t
ORIGIN

Query Match 77.4%; Score 546; DB 12; Length 832;
Best Local Similarity 92.4%; Pred. No. 9.1e-131;
Matches 597; Conservative 0; Mismatches 45; Indels 4; Gaps 2;

QY 62 CCTATGAATGACTAGCCACCTCGGTGTCAGTGTCCCTCCAGGACAGAC-GGCCAGGATC 120
Db 739 CCAATGTGTGACTAGCCACCTCGGTGTCAGTGTCCCTCCAGGACAGAGGAT 680
QY 121 ACCTGTGGGGGACACACAGTACAAATGAATATGTCTCACTGGTACCAGCAGAAGCCAGCG 180
Db 679 ACCTGTGGGGGCCCCAACATTGGAATTACAGTGTGCATGTGTACCAGCAGAAGTCAGGC 620
QY 181 CGGGCCCCCTATACTGTGTCTATCTATGATGATGATGACCGCCCTCAGGGATCCCTGAGCGA 240

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Db 619 CAGGCCCCCTGTCTGTCTATGATGATAGCGACCCGCCCTCAGGGATCCCTGAGCGA 560
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Db 559 TTCTCTGGCTCCAACTCTGGGAACACCGCCACCTGACCATCAGCAGGGTCCGAGCGGG 500
QY 301 GATGAGGCTGACTATTACTGTGAGTGGGACAGGGCTAGTGATCATCCGGT---CTTC 357
Db 499 GATGAGGCGCGACTATTACTGTGAGTGGTCCGATAGTGGTGTGATCATCTGTGCAATTC 440
QY 358 GGAGGAGGAGACCGGGGTGACCGTCTAGTTCAGCCCAAGGCTGCCCTCGGTCACTCTG 417
Db 439 GCGGAGGAGGACCAAACTGACCTGTAGGTTCAGCCCAAGGCTGCCCTCGGTCACTCTG 380
QY 418 TTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGGTGTCTCTATAAGT 477
Db 379 TTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGGTGTCTCTATAAGT 320
QY 478 GACTTCTACCCCGGAGCCGTGACAGTGGCTGGAGGCGAGTAGCAGCCCGTCAAGGCG 537
Db 319 GACTTCTACCCCGGAGCCGTGACAGTGGCTGGAGGCGAGTAGCAGCCCGTCAAGGCG 260
QY 538 GGAGTGGAGACCAACACACCCCTCCAAACAAAGCAACAAAGTACCGGCCAGCAGCTAC 597
Db 259 GGAGTGGAGACCAACACACCCCTCCAAACAAAGCAACAAAGTACCGGCCAGCAGCTAT 200
QY 598 CTGAGCTGACCCCTGAGCAGTGGAGTCCCAACAGAGCTACAGTGCACGAGTCAAGCAT 657
Db 199 CTGAGCTGACCCCTGAGCAGTGGAGTCCCAACAGAGCTACAGTGCACGAGTCAAGCAT 140
QY 658 GAAGGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT 703
Db 139 GAAGGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCAT 94

BQ884067 908 bp mRNA linear EST 16-AUG-2002
AGENCOURT_8616484 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302471
5', mRNA sequence.
BQ884067
VERSION BQ884067.1 GI:22276075
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2519 row: p column: 24
High quality sequence stop: 687.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:

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GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 205 a 277 c 231 g 167 t 28 others
ORIGIN

Query Match 77.4%; Score 545.8; DB 14; Length 908;
Best Local Similarity 91.5%; Pred. No. 1e-130;
Matches 590; Conservative 0; Mismatches 52; Indels 3; Gaps 1;
QY 62 CCTATGACATGCTCAGCCACCTCGGTGTCATGTCCTCCAGACAGAGCCGAGATCA 121
Db |||||
QY 72 CCCATGTTCTGACTCAGTCACCTCGGTGTCATGTCCTCCAGACAGAGCCGAGATCA 131
Db |||||
QY 122 CCGTGGGGAGACACAGTAGAATCAATATCTCCACTGGTACCAGCAGAGCCGAGCC 181
Db |||||
QY 132 CCGTGGGGAGACACATTTGGAAGTCAAGTGTGCACTGGTACCAGCAGAGCCGAGCC 191
Db |||||
QY 182 GGGCCCTTACTGCTGTCATCTATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGAT 241
Db |||||
QY 192 AGCCCTCTGTTGGTCTGCTAATGATAGACCGGCCCTCAGGGATCCCTGAGCGAT 251
Db |||||
QY 242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGCCGGGG 301
Db |||||
QY 252 TCTCTGGCTCCAACTCTGGGACACGCCACCTGGTCTCAGCAGGGTGAAGCCGACG 311
Db |||||
QY 302 ATGAGCTGACTATTACTGTCAGGTGTGGACAGGCGTAGTATCATC---CGTCTTCG 358
Db |||||
QY 312 ATGAGCCGACTATTACTGTCAGGTGTGGGATGATGATGATGATGATGATGATGAT 371
Db |||||
QY 359 GAGAGGGAGCCCGGTGACCGTCTAGGTGACGCCCAAGGCTGCCCTCGTCACTCTGT 418
Db |||||
QY 372 GCGAGGGACCAAGCTGACCGTCTAGGTGACGCCCAAGGCTGCCCTCGTCACTCTGT 431
Db |||||
QY 419 TCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGCCACACTGGTGTCTCATAGTG 478
Db |||||
QY 432 TCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGCCACACTGGTGTCTCATAGTG 491
Db |||||
QY 479 ACTTCTACCGGAGCCGTCAGAGTGGCTGGAGCAGATGACGCCCGCTCAAGCCG 538
Db |||||
QY 492 ACTTCTACCGGAGCCGTCAGAGTGGCTGGAGCAGATGACGCCCGCTCAAGCCG 551
Db |||||
QY 539 GAGTGGAGACCAACACACCTCCAAACAAAGCAACCAAGTACGCGGCCGAGCAGTACC 598
Db |||||
QY 552 GAGTGGAGACCAACACACCTCCAAACAAAGCAACCAAGTACGCGGCCGAGCAGTATC 611
Db |||||
QY 599 TGAGCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGTCCAGGTCAACGATG 658
Db |||||
QY 612 TGAGCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGTCCAGGTCAACGATG 671
Db |||||
QY 659 AAGGGAGCACCTGGAGAGACAGTGGCCCTACAGATGTTTAT 703
Db |||||
QY 672 AAGGGAGCACCTGGAGAGACAGTGGCCCTACAGATGTTTAT 716
Db |||||

RESULT 11
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DEFINITION 60369019F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217796 5', mRNA sequence.
ACCESSION BI907909
VERSION BI907909.1 GI:16170804
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 754)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Cloned through the I.M.A.G.E. Consortium information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1547 row: f column: 05
High quality sequence stop: 749.

FEATURES

Location/Qualifiers
1..754
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/db_xref="taxon:9606"
/clone="IMAGE:5217796"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
BASE COUNT 167 a 239 c 210 g 138 t
ORIGIN

Query Match 77.4%; Score 545.6; DB 13; Length 754;
Best Local Similarity 89.4%; Pred. No. 1e-130;
Matches 622; Conservative 0; Mismatches 69; Indels 5; Gaps 3;
QY 10 CCGCTCAGCTCCTCGGGCTCTCTGCTCCAGGTGCAGATGTCCTATGAA 69
Db |||||
QY 38 CCGGTTCTCTCTCGGGCTCTCTCTCACTG---CACAGCCTCTGTAACTCTATGTG 94
Db |||||
QY 70 CTGACTCAGCCACCTCGGTGTGTCCTCCAGACAGAGCCGAGGATCACTGTGG 129
Db |||||
QY 95 CTGACTCAGCCACCTCGGTGTGTCAGGGCCCAAGACAGAGCCGAGGATGAGGC 154
Db |||||
QY 130 GGAGACACAGTAGAATGATATGTCCATGTTACAGCAGAGCAGCGGGCCCT 189
Db |||||
QY 155 GGAGACACAGTCGAACATAAACTGTGCACTGGTACCAGCAGAGCAGCGGCCCT 214
Db |||||
QY 190 ATACTGTCATCTATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATCTTGGC 249
Db |||||
QY 215 GTATTGGTCTATGATGATACCGCGGGCTCAGGGATCCCTGACCGATTTCTTGGC 274
Db |||||
QY 250 TCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGTGAGGCCGGGATGAGGCT 309
Db |||||
QY 275 TCCAAATCTGGGACACAGGCCACCTGACCGTACAGGGTCAAGCCGGGATGAGGCC 334
Db |||||
QY 310 GACTATTACTGTGAGGTGGGACAGGGCTAGTGTATCATCCGGTCTTCGAGAGGAGACC 369
Db |||||
QY 335 GACTATTATTGTGAGGTGGGATAGTGTATGATCATTTGGTGTTCGCGGAGGAGCC 394
Db |||||
QY 370 CCGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCGCCCTCC 429
Db |||||
QY 395 AGGCTGACCGCTCTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCGCCCTCC 454
Db |||||
QY 430 TCTGAGGAGCTTCAAGCCCAAGGCCACACCTGGTGTCTCATAGTCACTTCTACCCG 489
Db |||||
QY 455 TCTGAGGAGCTTCAAGCCCAAGGCCACACCTGGTGTCTCATAGTCACTTCTACCCG 514
Db |||||
QY 490 GGAGCCGTGACAGTGGCTGGAGG-CGAGATAGCAGCCCGCTCAAGCGGGAGTGAGAC 548
Db |||||
QY 515 GGAGCCGTGACAGTGGCTGGAGGAGCAGATAGCAGCCCGCTCAAGCGGGAGTGAGAC 574
Db |||||
QY 549 CACACACCTCTCAACAAAGCAACAAAGTACGGGCCAGCAGCTACTGAGCTGAC 608
Db |||||

Db 575 CACRACACCTCCAAACAAAGCAACAAGTACGGCCAGCAGCTACTGAGCCTGAC 634
 QY 609 GCTGTAGAGTGGAAGTCCACAGAGCTACA-GTGCAGGTTCAGCATGATGAGGAGCA 667
 Db 635 GCTGTAGAGTGGAAGTCCACAAAGCTACAGGTGCGAGGTACGATGAAGGAGCA 694
 QY 668 CCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 703
 Db 695 CCGTGGAGAGACAGTGGCCCTACAGATGTTTCAT 730

RESULT 12
 BG756256
 LOCUS
 DEFINITION
 mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1700 row: 9 column: 18
 High quality sequence stop: 786.
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 /clone="IMAGE:4853801"
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC library."
 226 a 272 c 257 g 169 t

BASE COUNT
 ORIGIN

Query Match 77.3%; Score 545.2; DB 12; Length 924;
 Best Local Similarity 92.7%; Pred. No. 1.5e-130;
 Matches 595; Conservative 0; Mismatches 43; Indels 4; Gaps 2;
 QY 62 CCTATGAATGACTCAGCACCCCTCGGTGTCAAGTGTCCCGCAGCAGAGCGGCAGGATCA 121
 Db 14 CCTATGTGTGACTCAGCACCCCTCGGTGTCAAGTGTCCCGCAGCAGAGCGGCAGGATTA 73
 QY 122 CTTGTGGGGAGACAAACAGTAGAATATGTCACATGTGTGTCACGACGAGAGCCAGCCG 181
 Db 74 CTTGTGGGGAGACAAACATTGGAAGTAAAGTGTGCACTGGTATCAGCAGAGGCGAGCC 133
 QY 182 GGGCCCCCTACTGGTCACTATGATAGTACCGGCCCTCAGGATCCCTGACCGAT 241
 Db 134 AGGCCCCCTGTGGTGTGCTATGAAAGATAGTAGACCGGCCCTCAGGATCCCTGAGCGAT 193

QY 242 TCTTGGGTCCAAATCAGGGAACACCGCCACCCCTGACCATCAACGGGGTTCGAGCGCGGG 301
 Db 194 TCTTGGGTCCAACTCTGGGAACACCGCCACCCCTGACCATCAACGGGGTTCGAGCGCGGG 253
 QY 302 ATGAGGCTGACTATTACTGTGAGGTGTGGGACAGGGCTAGTGCATCATCGGTCTTCGGAG 361
 Db 254 ATGAGGCGGACTATTACTGTGAGGTGTGGGATAGAAAGTAGTG---ATGTAGTATTTCGGCG 310
 QY 362 GAGGACCCGGGTGACCGTCTCTAGGTACAGCCCAAGCGTGCCTCGGTCTCGGTCACTCTGTTC 421
 Db 311 GAGGACCAAGCTGACCGTCTGTAGTACAGCCCAAGCGTGCCTCGGTCACTCTGTTC 370
 QY 422 GCGCCTCTCTGAGAGCTTCAAGCAACAAGGCCACACTGTGTGTCTCTCATAAGTGA 481
 Db 371 GCGCCTCTCTGAGGAGTTCAAAGCAACAAGGCCACACTGTGTGTCTCTCATAAGTGA 430
 QY 482 TCTACCCGGGAGCCGTGACAGTGGCTCGAAGGCGAGTAGCAGCCCGTCAAGGGCGGAG 541
 Db 431 TCTACCCGGGAGCCGTGACAGTGGCTCGAAGGCGAGTAGCAGCCCGTCAAGGGCGGAG 490
 QY 542 TGGAGACCAACACACCCCTCCAAACAAAGCAACAAGTACCGGCCAGCAGCTACTCA 601
 Db 491 TGGAGACCAACACACCCCTCCAAACAAAGCAACAAGTACCGGCCAGCAGCTACTCA 550
 QY 602 GCTGACCGCTGAGCAGTGGAAAGTCCCACAGAACTACAGTGCAGGTCACGCTAAGA 661
 Db 551 GCTGACCGCTGAGCAGTGGAAAGTCCCACAGAACTACAGTGCAGGTCACGCTAAGA 610
 QY 662 GGAGCACCGTGGAGAGACAGTGGCCCTCAGCAATGTTTCAT 703
 Db 611 GGAGCACCGTGGAGAGACAGTGGCCCTCAGCAATGTTTCAT 651

RESULT 13

BG924274
 LOCUS
 DEFINITION
 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12807 row: k column: 16
 High quality sequence stop: 710.
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 BM924274
 BM924274.1 GI:19374641
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12807 row: k column: 16
 High quality sequence stop: 710.
 Location/Qualifiers
 1. .1086
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5760519"
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 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon, 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is

FEATURES
 source

1. .1086
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5760519"
 /clone_lib="NIH MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon, 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."

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BASE COUNT      255 a  355 c  270 g  199 t
ORIGIN

Query Match      77.3%; Score 545; DB 14; Length 1086;
Best Local Similarity 88.0%; Pred. No. 1.8e-130;
Matches 603; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

QY 19 CTCCTGGGGCTCCTGCTGCTCTGGCTCCAGGTGACGATGCTGCTATGAATGACTCAG 78
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Db 55 CTCCTCTCGGCTCTCTCTCACTGACAGGCTCTTGACCTCTATGCTGACTCAG 114
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QY 79 CCACCTCGGTGTCAGTGTCCCGAGACAGAGCGCCAGGATCACCTGTGGGGAGACAAC 138
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Db 115 CCACCTCGGTGTCAGTGTCCCGAGAGAGAGCGCCAGGATTAACCTGT- GGGGAAACTAC 173
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QY 139 ACTAGAAATCAATATCTCCACTGTGTACGACGAGAGCCAGCGCGGCCCTTACTGTGTC 198
   |||||
Db 174 ATTAGAGGTACAGTGTGCACTGTGTACCGGACGACGCGCGGCCCTGTATTGGCC 233
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QY 199 ATCTATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAAATCA 258
   |||||
Db 234 GTCTACGATGATAACCGCGGCCCTCAGGATCCCTGCGGATTCGCTGCTCCAAGTCT 293
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QY 259 GGGAAACACGCCCACTCTGACCAATCAACCGGGTTCGAGCGCGGGATGAGGTGACTATTAC 318
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Db 294 GAAACACAGCCCACTCTGACCAATCAGCAGGGTTCGAGCGCGGGATGAGGCGCACTATTAC 353
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QY 319 TGTCAAGTGTGGACAGGGCTAGTGATCATCCGGTCTTCGAGGAGGAGCCCGGTGACC 378
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Db 354 TGTCAAGTGTGGACAGGGCTATAGTATCATTTGGTGTTCGCGGAGGAGCAAGCTGACC 413
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QY 379 GTCTAGGTGAGCCCAAGGCTGCGCCCTCGGTCACTCTGTTCGCGCCCTCTCTGAGGAG 438
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Db 414 GTCTAGGTGAGCCCAAGGCTGCGCCCTCGGTCACTCTGTTCGCGCCCTCTCTGAGGAG 473
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QY 439 CTTCAAGCCCAACGAGGCACTGTGTGTCTCATAGTGAATTTACCGGGAGCCGTG 498
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QY 559 TCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACTGAGCCTGACGCTGAGCAG 618
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QY 619 TGAAGTCCCAAGAGGTACAGCTCCAGGTCAACGATGAAGGGAGCAACCGTGGAGAAG 678
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Db 654 TGAAGTCCCAAGAGGTACAGCTCCAGGTCAACGATGAAGGGAGCAACCGTGGAGAAG 713
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QY 679 ACAGTGGCCCTACAGATGTTTCAT 703
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RESULT 14
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DEFINITION AGENCOURT_8475231 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301461
5', mRNA sequence.
ACCESSION BO711587
VERSION BO711587.1 GI:21850486
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 917)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2517 row: f column: 22
High quality sequence stop: 552.

FEATURES
source

Location/Qualifiers
1..917
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/db_xref="taxon:9606"
/clone="IMAGE:6301461"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

BASE COUNT 223 a 286 c 242 g 166 t

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Query Match      77.2%; Score 544.4; DB 14; Length 917;
Best Local Similarity 88.5%; Pred. No. 2.4e-130;
Matches 614; Conservative 0; Mismatches 76; Indels 4; Gaps 2;

QY 11 CGCTCAGTCTCTGGGGCTCCTGCTGCTCTGGCTCCAGGTGACGATGCTGCTATGAAC 70
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QY 131 GAGACAAAGTAGAATGAATATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
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QY 191 TACTGCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
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Db 215 TCTGCTGCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 274
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QY 251 CCAATACAGGGAACACCGCCACCTTGACCATCAACGGGGTCCAGGCGGGGATGAGGCTG 310
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Db 275 CCACCTCTGCTGATACGGCCACCTTGACCATCAACGGGGTCCAGGCGGGGATGAGGCGG 334
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QY 311 ACTATTACTGTGAGGTGTGGGACAGGGGTAGTATCATCCGGTCTTCGAGGAGGAGCC 370
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QY 371 GGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCGCCCTCTCT 430
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Db 395 GGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCGCCCTCTCT 454
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RESULT 15

BQ709509
 LOCUS
 DEFINITION BQ709509 949 bp mRNA linear EST 16-JUL-2002
 AGENCOURT 8418138 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281593
 5', mRNA sequence.

ACCESSION BQ709509
 VERSION BQ709509.1 GI:21848408
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 949)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Cloning by: Agencourt Bioscience Corporation

Cloning distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2474 row: k column: 02

High quality sequence stop: 635.

Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
 /clone="IMAGE:6281593"
 /clone_lib="NIH MGC 113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
 BASE COUNT 221 a 301 c 247 g 179 t 1 others
 ORIGIN

Query Match

Best Local Similarity 76.9%; Score 542.4; DB 14; Length 949;
 Matches 614; Conservative 88.2%; Pred. No. 8e-130;

Mismatches 76; Indels 6; Gaps 2;

QY 11 CCCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCAGGTGCAGCATGTCCTATGAAC 70

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DB 26 CCGTCTCTCTCGGCTCCTCTCTCACTG---CACAGCTCTGTGACCTCTATGTGC 82

|||||

QY 71 TGACTCAGCACCTCGGTGTCACTGTCCAGGACAGCGCCAGGATCACCTGTGGG 130

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DB 83 TGACCCAGCACCTCGGTGTCCGTCGTCGCGCCAGGACAGCGCCAGATTCGCTGTGAA 142

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QY 131 GAGACACAGTAGAATGATGTCTCACTGGTACAGAGAGCCAGCGCGGCCCTTA 190

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|||||

|||||

|||||

|||||

|||||

DB 143 GAAACAGATTGAAGTAGCATATATAAAGTGGTACCAAGAGCCAGCGCCGCGCTG 202
 QY 191 TACTGGTCAATCATATGATAGTACCGGCCCTCTAGGGATCCCTGAGCGAATCTCTGGCT 250
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 QY 428 CCTCTGAGGAGCTTCAAGCCCAAGGCTGGTGTGTCTCATAGTGAATCTTCTACC 487
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Job time : 967.424 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:14:13 ; Search time 157.546 Seconds
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10077.457 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	18 AAT62509	Primates anti-hu
2	705	100.0	705	19 AAV35484	Macaque primatized
3	705	100.0	705	24 AAS17242	DNA sequence of a
4	585.2	83.0	702	18 AAT62867	Ant-CD4 monkey-hu
5	582.6	82.6	926	20 AA224427	Human bladder tumor
6	555.6	78.8	836	23 AAS83482	DNA encoding novel
7	540.2	76.6	711	19 AAV35488	Macaque primatized
8	540.2	76.6	711	24 AAS17246	DNA sequence of a
9	538.6	76.4	711	18 AAT62512	Primates anti-hu

10	527.6	74.8	1027	24	ABQ54438	Human ovarian anti
11	524	74.3	841	23	AAS83486	DNA encoding novel
12	520.8	73.9	904	24	ABK28671	Human CDNA encoding
13	520.4	73.8	869	22	AAS22717	Human CDNA encoding
14	516	73.2	791	23	AAS82771	DNA encoding novel
15	515	73.0	1825	22	AAS22777	Human CDNA encoding
16	514.4	73.0	859	22	AAS22481	Human CDNA encoding
17	512.8	72.7	960	21	AAC78188	Human cancer assoc
18	512	72.6	872	9	AAN81655	VDJC regions of hu
19	511	72.5	654	22	AAS13364	Human CDNA encoding
20	509.2	72.2	930	22	AAS22541	Human CDNA encoding
21	506	71.8	793	23	AAS83481	DNA encoding novel
22	504	71.5	807	23	AAS83484	DNA encoding novel
23	495.2	70.2	863	24	ABK28650	Human CDNA encoding
24	480	68.1	849	22	AAH98186	Human EST-derived
25	474.2	67.3	884	11	AAQ03609	Sequence encoding
26	473.6	67.2	810	23	AAS87270	DNA encoding novel
27	473	67.1	935	22	AAC66525	Human immune syste
28	472	67.0	768	20	AAK06953	Monoclonal antibod
29	472	67.0	768	20	AAK06954	Monoclonal antibod
30	465.6	66.0	826	22	AAI58109	Human polynucleoti
31	462.8	65.6	915	24	ABN97248	Gene #3746 used to
32	462.8	65.6	915	24	ABK64815	Human benign prost
33	462.8	65.6	915	24	ABL65478	Lung cancer relate
34	462.2	65.6	654	14	AAQ49835	Anti-HIV-1 recombi
35	462	65.5	762	22	AAC84209	Plasmid Glambda-1B
36	462	65.5	5679	22	AAK4207	DNA encoding novel
37	461.8	65.5	889	23	AAS77073	DNA encoding novel
38	457	64.8	902	14	AAQ35100	Antibody D lambda
39	456	64.7	895	22	AAC66530	Human immune syste
40	455.6	64.6	763	23	AAS83480	DNA encoding novel
41	455.4	64.6	891	22	AAC66528	Human immune syste
42	455.2	64.6	708	22	AAH47902	Human type antihum
43	453.6	64.3	783	23	AAS83483	DNA encoding novel
44	452	64.1	876	23	AAS83478	DNA encoding novel
45	451.6	64.1	651	19	AAV11293	Antibody HB4C5 lig

ALIGNMENTS

RESULT 1
AAT62509
ID AAT62509 standard; DNA; 705 BP.
XX AC
XX AAT62509;
XX DT 25-MAY-1997 (first entry)
XX DE
XX DE Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA.
XX KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
XX KW Primatised antibody; B7 antigen; CD28; immunosuppressive;
XX KW autoimmune disease; idiopathic thrombocytopenia purpura;
XX KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
XX KW type 1 diabetes mellitus; graft versus host disease;
XX KW hetero-hybridoma; transfectoma; ss.
XX OS Chimeric Macaca cynomolgus;
XX OS Chimeric Homo sapiens.
XX PN WO9640878-A1.
XX PD 19-DEC-1996.
XX PF 06-JUN-1996; 96WO-US10053.
XX PR 07-JUN-1995; 95US-0487550.
XX PA (IDEC-) IDEC PHARM CORP.
XX XX Anderson DR, Brans P, Hanna N, Shestowsky WS;
XX XX

Qy	361	GGAGGACCGGGTGACCGTCTCAGGTGAGCCGCAAGGCTGCCCTCGGTCACTCTGTTC	421
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Qy	481	TTCTACCCGGGAGCGTGACGTGGCGCTTGGAGGCAAGTAGACGCCCGCTCAGGCGGGA	540
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Qy	541	GTGGAGACCAACACACCTCTCCAAACAAAGCAACACAAAGTACGGGGCCAGCAGCTACCTG	600
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Qy	601	AGCCTGACGCCCTGAGCAGTGGAGTCCACACAGACTACAGCTGCCAGGTTCAGCATGAA	660
Db	601	AGCCTGACGCCCTGAGCAGTGGAGTCCACACAGACTACAGCTGCCAGGTTCAGCATGAA	660
Qy	661	GGGAGCACCGTGAGGAAGACAGTGGCCCTTACAGAAATGTTTCATGA	705
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RESULT 4	
AAT62867	AAT62867 standard; DNA; 702 BP.
XX AC	
XX AC	AAT62867;
XX XX	
DT DT	18-OCT-1997 (first entry)
XX XX	
DE DE	Ant-CD4 monkey-human chimeric antibody CB9.1 DNA.
XX XX	
XX KW	CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW KW	cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW KW	leukaemia; lymphoma; graft-versus-host disease; asthma;
KW KW	transplant rejection; HIV; therapy; CB9.1; ss.
XX XX	
OS OS	Chimaeric Macaca cynomolgus;
XX OS	Chimaeric Homo sapiens.
XX PN	WO9709351-A1.
XX PD	13-MAR-1997.
XX PF	05-SEP-1996; 96WO-US14324.
XX PF	
XX PR	06-SEP-1995; 95US-0523894.
XX XX	
PA PA	(IDEC-) IDEC PHARM CORP.
XX XX	
PI PI	Hanna N, Newman RA, Reff ME;
XX XX	
DR DR	WPI; 1997-201913/18.
DR DR	P-PSDB; AAW14924.
XX XX	
PT PT	Chimeric antibody comprising monkey variable domains and human
PT PT	constant domains - affects CD4-mediated immune functions, esp.
PT PT	useful for treatment of autoimmune disease, e.g. rheumatoid
PT PT	arthritis
XX XX	
FS FS	Example 1; Page 79-80; 155pp; English.
XX XX	
CC CC	A DNA sequence (AAT62867) codes for lambda variable and constant
CC CC	domains (AAW14924) of anti-human CD4 monkey/human chimeric antibody
CC CC	CB9.1. This antibody contains the antigen binding domains (see
CC CC	also AAW14922-23) of a cynomolgus monkey anti-CD4 monoclonal
CC CC	antibody, a human heavy chain constant region of gamma 1 isotype
CC CC	and Gm1a, Gm1z allotype, and a human lambda light constant region
CC CC	of the Oz minus, mcg minus genotype and Ke minus allotype. The
CC CC	immunoglobulin genes were cloned into mammalian expression vector

CC	TCAE 6, and chimeric antibody was produced in CHO cells. CE9.1 binds to domain 1 of human, but not macaque, CD4, a region involved in the interaction with MHC Class II molecules on antigen-presenting cells. It shows potent immunomodulatory activity with low immunogenicity in humans, and can be used to treat autoimmune diseases such as rheumatoid arthritis.
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SQ	Sequence 702 BP; 151 A; 217 C; 207 G; 127 T; 0 other;
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Best Local Similarity	89.6%; Pred. No. 4.2e-137;
Matches 629; Conservative	0; Mismatches 73; Indels 0; Gaps 0;
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Db	
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Qy	64 TATGAAGTACTCAGCACCCCTCGGTGTCCCAGGACAGAGCGGCAGGATCACC 123
Db	
Db	61 TATGAGTTGAGTCAGACCTCGCTCAGTGTCCGTGTCCCAGGACAGAGCGCGGTTCACC 120
Qy	124 TGTTGGGGGACACAACAGTAGAATAATGATGTCCTACTGTGTACCAGAGAAGCCAGCGCGG 183
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Db	121 TGTTGGGGGACACAACGTTTGAAGAAAGTTACAGTGTACGAGAGAAGCCACGCAG 180
Qy	184 GCCCTATACTGGTCTATATGATGATGAGACCGGCCCTCAGGGATCCCTGAGCGATTTC 243
Db	
Db	181 GCCCTGTGTGCTGCTATCTATGCTGACAGGAACGCCCTCAGGGATCCCTGCGCATTC 240
Qy	244 TCTGGCTCAAATCAGGGAACACGGCCACCCCTGACCATCAACGGGGTTCAGGCCGGGGAT 303
Db	
Db	241 TCTGGCTCCAACCTCAGGGAACACCGCCACCCCTGACCATCAGCGGGTTCGAGGCCGGGGAT 300
Qy	304 GAGGCTGACTATTACTGTCTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTTCGGAGGA 363
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Qy	364 GGGAACCCGGGTGACCGCTCTAGTGTACGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG 423
Db	
Db	361 GGGAACCCGGGTGACCGCTCTAGTGTACGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG 420
Qy	424 CCCTCTCTCAGGAGCTTCAAGCCACAAGGCCACACTGGTGTGTCTCATAGTGACTTTC 483
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Db	421 CCCTCTCTCAGGAGCTTCAAGCCACAAGGCCACACTGGTGTGTCTCATAGTGACTTTC 480
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Db	481 TACCGGGAGCCGTGACAGTGGCTGGAAGGCAGATAGCAGCCCGCTCAAGCGCGGAGTG 540
Qy	544 GAGACCAACACACCCCTCCAAACAAAGCAACAACAGTAGCGCGCCAGCAGTACCTTGAGC 603
Db	
Db	541 GAGACCAACACACCCCTCCAAACAAAGCAACAACAGTAGCGCGCCAGCAGTACCTTGAGC 600
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Db	
Db	601 CTGACGCTCAGCAGTGGAGTCCCACAGAAGCTACAGTGCAGGTCCAGCATGCAAGAGG 660
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Db	
Db	661 AGCACCGTGGAGAAGACAGTGGCCCTACAGATGTTTCATGA 702
<hr/>	
RESULT 5	
AAZ24427	
ID	AAZ24427 standard; cDNA; 926 BP.
XX	
XX	AAZ24427;
XX	
DT	14-FEB-2000 (first entry)
XX	
DE	Human bladder tumour cDNA library derived EST 39.
XX	
XX	Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;

CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AA564197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 836 BP; 185 A; 262 C; 232 G; 157 T; 0 other;

Query Match 78.8%; Score 555.6; DB 23; Length 836;
 Best Local Similarity 91.6%; Pred. No. 1.1e-129;
 Matches 588; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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QY 122 CCTGTGGGGAGACACAGTAGAATGAATATGTCACCTGTTACCGAGCAAGCCGCGC 181
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QY 182 GCGCCCTTACTACTGCTATCATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGAT 241
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QY 362 GAGGAGCCCGGTGACCGTCTAGTTCAGCCCAAGGCTGCCCTCGGTCACTGTCTTC 421
 |||||
 Db 401 GAGGACCAAGCTGACCGTCTTGGTCAGCCCAAGGCTGCCCTCGGTCACTGTCTTC 460
 |||||

QY 422 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGCTGTGTCTCATAGTGACT 481
 |||||
 Db 461 CGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGCTGTGTCTCATAGTGACT 520
 |||||

QY 482 TCTACCGGAGCGGTGACAGTGGCTGGAAGCAGATAGACGCCCGTCAAGCGCGGAG 541
 |||||
 Db 521 TCTACCGGAGCGGTGACAGTGGCTGGAAGCAGATAGACGCCCGTCAAGCGCGGAG 580
 |||||

QY 542 TGGAGACCAACACACCTCCAAACAAAGCAACAGTACGCGGCGCAGCAGTACTCTGA 601
 |||||
 Db 581 TGGAGACCAACACACCTCCAAACAAAGCAACAGTACGCGGCGCAGCAGTACTCTGA 640
 |||||

QY 602 GCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGTCCAGGTCAACGATGAAG 661
 |||||
 Db 641 GCCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGTCCAGGTCAACGATGAAG 700
 |||||

QY 662 GGAGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCAAT 703
 |||||
 Db 701 GGAGCACCGTGGAGAAACAGTGGCCCTTACAGATGTTTCAAT 742
 |||||

RESULT 7

AAV35488
 ID AAV35488 standard; DNA; 711 BP.

XX AC
 XX AAV35488;

XX 29-SEP-1998 (first entry)

XX Macaque primatized 16C10 light chain DNA.

XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation; ss.

XX Macaca fascicularis.
 XX Key Location/Qualifiers
 FH 1..711
 FT /tag= a
 FT /product= 16C10 light chain

XX PN W09819706-A1.

XX PD 14-MAY-1998.

XX PF 29-OCT-1997; 97WO-US19906.

XX PR 08-NOV-1996; 96US-0746361.

XX PA (IDEC-) IDEC PHARM CORP.

XX PI Anderson DR, Brans P, Hanna N;

XX DR P-PSDB; AAW63764.

XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 CC inhibiting binding to CD28 - useful as specific immunosuppressants
 CC for treating diseases that involve interactions between T and B
 CC cells, e.g. graft rejection or tumours

XX Example 7; Fig 5a; 87pp; English.

XX This sequence encodes a primatized form of the antibody 16C10 light chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.

XX SQ Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match 76.6%; Score 540.2; DB 19; Length 711;
 Best Local Similarity 86.1%; Pred. No. 7.8e-126;
 Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCAGTGCCAGATGT 60
 |||||
 Db 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCAGTGCCAGATGT 60
 |||||

QY 61 GCCTATGAATGACTCAGCCACCTCGGTGTCTAGTGTCTCCAGGACAGCGGCCAGATC 120
 |||||
 Db 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGGCCCGCCAGGCGAGAGGTTCACCATC 120
 |||||

QY 121 ACCTGTGGGGG-----AGACAACAGTAGAATATGATGTCTCCACTGGTACCAGCAGAAG 174
 |||||

Db 121 TGTGTCACTGGGAGACACCTCCAACTGGAGTTATGATCTATCTGTTGTTACAGCAGCTC 180
 |||||

QY 175 CCAGCGCGGGCCCTTACTACTGTCTATGATGATAGTACCGGCCCTCAGGATCCCT 234
 |||||

Db 181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGGACCCCTCAGGAATTTCT 240
 |||||

QY 235 GAGCGATTTCTGGTCCCAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAG 294
 |||||

PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Birse CE, Rosen CA;	
XX		
DR	WPI; 2002-147878/19.	
DR	P-PSDB; ABP41361.	
XX		
PT	Isolated nucleic acid molecules encoding novel ovarian polypeptides,	
PT	useful in the prevention, treatment and diagnosis of cancer (e.g.	
PT	ovarian cancer), immune disorders, cardiovascular disorders and	
PT	neurological diseases -	
XX		
PS	Claim 1; SEQ ID No 318; 2922pp; English.	
XX		
CC	The invention relates to 2175 novel human ovarian antigens (ABP41054-	
CC	ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also	
CC	encompasses polypeptides 90% identical and polynucleotides 95% identical	
CC	to the sequences of the invention. The invention additionally relates to	
CC	recombinant vectors and host cells comprising human ovarian antigen	
CC	polynucleotides, antibodies against human ovarian antigens, and the use	
CC	of ovarian antigen polynucleotides and polypeptides in diagnosing,	
CC	treating, prognosing or preventing various ovary and/or breast-related	
CC	disorders. Such conditions include ovarian cancer and breast cancer, and	
CC	metastatic tumours of ovarian or breast origin, reproductive system	
CC	disorders (e.g., infertility, disorders of pregnancy, anovulation,	
CC	polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine	
CC	disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic	
CC	shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and	
CC	vaginitis), immune disorders (e.g., congenital and acquired	
CC	immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),	
CC	blood-related disorders (e.g., anaemia), cardiovascular disorders,	
CC	respiratory disorders, neurological disorders, gastrointestinal disorders	
CC	and urinary system disorders. Ovarian antigen polypeptides and	
CC	polynucleotides may also be used in screening for compounds which	
CC	modulate ovarian antigen expression or activity. The polynucleotides may	
CC	further be used for gene therapy, chromosome mapping, in the	
CC	identification of individuals and in forensic analysis, and the	
CC	polypeptides may be used as food additives or to prepare antibodies	
CC	useful in disease diagnosis, drug targeting and phenotyping. The present	
CC	sequence represents cDNA encoding a human ovarian antigen of the	
CC	invention.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences .	
XX		
SQ	Sequence 1027 BP; 253 A; 306 C; 264 G; 192 T; 12 other;	
	Query Match: 74.8%; Score 527.6; DB 24; Length 1027;	
	Best Local Similarity 89.7%; Pred. No. 1.2e-122;	
	Matches 576; Conservative 3; Mismatches 57; Indels 6; Gaps 1;	
QY	62 CCTATGAACCTGACTCAGCCACCCCTCGGTGTCACTGTCCCGCAGCAGAGCGCCGAGTCA 121	
DB	192 CCTATGAGTGTACTCAGCACCCCTCAGTGTCCGTGTCGCCGAGCAGCAGCAGTCA 251	
QY	122 CTGTGGGGAGACAAAGTAGAAATATGATATGTCACCTGGTACCGAGAGAGCCAGCC 181	
DB	252 CTGCTCTCGAGATAAATTGGGGGATAAATATCTTGTGTATCAGCAGAGCCAGGCC 311	
QY	182 GGGCCCTATACGTGTATCTATGATAGTAGTACCGGCCCTCAGGATCCCTGACGAT 241	
DB	312 AGTCCCTGTGTGTGTCATCTATCAAGATAACACGGCCCTCAGGATCCCTGACGAT 371	
QY	242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGCCGGG 301	
DB	372 TCTCTGGCTCCAACTTGGGACACAGCCACTCTGACCATCAGCGGAGCCAGGCTATGG 431	
QY	302 ATGAGGTGACTATTTACTGTGAGTGTGGGACAGGCTAGTATCATCCGGTCTTCGGAG 361	
DB	432 ATGAGGTGACTATTTACTGTGAGGCGTGGGACAGCAGCACTG-----KGGTATTCGGG 485	
QY	362 GAGGAGCCGGGTGACCGTCTTAGTTCAGGCCAGAGCTGCCCTCGGTCACTCTCTTCC 421	

Db	486 GAGGACCAAGCTGACCGTCTTAGTTCAGCCCAAGGCTGCCCTCGGTCACTCTCTTCC 545
QY	422 CGCCCTCTCTCGAGGAGCTTCAAGCCAAACAGGCCACACTGGTGTGTCTCTATAAGTACT 481
Db	546 CGCCCTCTCTCGAGGAGCTTCAAGCCAAACAGGCCACACTGGTGTGTCTCTATAAGTACT 605
QY	482 TCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGCAGCCCTCAAGGGCGGAG 541
Db	606 TCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCGAGATAGCAGCCCTCAAGGGCGGAG 665
QY	542 TGGAGACACACACACCTCCAAACAAAGCAACAAAGTACCGCGGCACAGCTACTCTGA 601
Db	666 TGGAGACACACACACCTCCAAACAAAGCAACAAAGTACCGCGGCACAGCTACTCTGA 725
QY	602 GCTTCAGCGCTGAGCAGTGGAGTCCCAAGAGCTTACAGCTGCCAGGTTCAGCCATGAAG 661
Db	726 GCTTCAGCGCTGAGCAGTGGAGTCCCAAGAGCTTACAGCTGCCAGGTTCAGCCATGAAG 785
QY	662 GGAGCACCGTGGAGAGACAGTGGCGCCCTACAGATGTTTCAT 703
Db	786 GGAGCACCGTGGAGAGACAGTGGCGCCCTACAGATGTTTCAT 827

RESULT 11

AAS83486

ID AAS83486 standard; cDNA; 841 BP.

XX

AC AAS83486;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #19290.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO2001/5067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

XX

 PT | New isolated polynucleotide and encoded polypeptides, useful in || PT | diagnostics, forensics, gene mapping, identification of mutations |
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	
PS	Claim 1; SEQ ID No 19290; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS94197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 841 Bp: 191 A: 273 C: 224 G: 153 T: 0 other:

KW	muscular active general; anticonvulsant; nootropic; neuroprotective;
KW	anti allergic; hypertensive; cardiovascular disorder; atherosclerosis;
KW	hypertension; myocardial infarction; autoimmune disorder;
KW	inflammatory disorder; AIDS; acquired immunodeficiency syndrome;
KW	allergy; rheumatoid arthritis; cell proliferative disorder; cancer;
KW	developmental disorder; Duchenne muscular dystrophy;
KW	neurological disorder; epilepsy; Alzheimer's disease.
XX	
XX	Homo sapiens.
XX	WO2001198353-A2.
PN	
XX	
PD	27-DEC-2001.
XX	
PF	20-JUN-2001; 2001WO-US19862.
XX	
PR	20-JUN-2000; 2000US-212890P.
PR	23-JUN-2000; 2000US-213456P.
PR	27-JUN-2000; 2000US-214601P.
PR	31-JUL-2000; 2000US-222372P.
PR	08-SEP-2000; 2000US-231435P.
PR	15-SEP-2000; 2000US-232889P.
XX	
XX	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Hillman JL, Tang YT, Yue H, Elliott VS, Tribouley CM, Lee EA;
PI	Ramkumar J, Lal P, Xu Y, Warren BA, Hafalia AJA, Baughn MR;
PI	Asimzai Y, Batra S, Burford N, Yao MG, Nguyen DB, Lu DM;
PI	Walia NK, Gandhi AR, Au-Young J, Patterson C;
XX	
DR	WPI; 2002-090431/12.
DR	P-PSDB; AAU82012.
XX	
PT	Forty four human secreted proteins (referred to as SSCP-1 to SSCP-44),
PT	useful in the diagnosis, treatment and prevention of cardiovascular
PT	(e.g. atherosclerosis), autoimmune/inflammatory (e.g. allergies) and
PT	cell proliferative disorders -
XX	
PS	Claim 5; Page 190; 195pp; English.
XX	
CC	The invention relates to forty four human secreted proteins (referred to
CC	as SSCP-1 to SSCP-44) and the nucleic acids encoding them. Also
CC	included are a host cell transformed with the nucleic acid, a
CC	transgenic animal comprising the nucleic acid, an anti-SSCP
CC	antibody, use of the SSCP proteins in isolating agonists and antagonists
CC	of SSCP activity and a method of isolating compounds which alter the
CC	expression of the SSCP nucleic acid. The SSCP polynucleotides and
CC	polypeptides are useful in the diagnosis, treatment and prevention of
CC	cardiovascular (e.g. atherosclerosis, hypertension, myocardial
CC	infarction), autoimmune/inflammatory (e.g. acquired immunodeficiency
CC	syndrome (AIDS), allergies, rheumatoid arthritis), cell proliferative
CC	(e.g. cancer), developmental (e.g. Duchenne and Becker muscular
CC	dystrophy), and neurological (e.g. epilepsy, Alzheimer's disease)
CC	disorders. Numerous other examples of each disorder are given in the
CC	specification. The present sequence is a cDNA encoding a SSCP protein.
XX	
SO	Sequence 904 BP: 225 A; 281 C; 231 G; 167 T; 0 other;

	Query Match	73.9%	Score 520.8	DB 24	Length 904
	Best Local	Similarity 84.0%	Pred. No. 6e-121		
	Matches 588	Conservative 0	Mismatches 112	Indels 0	Gaps 0
Qy	4	AGGGTCCCCGCTCAGCTCTCTGGGGCTCCCTGCTGCTCTGGCTCCAGGTGACGATGTGCC	63		
Db	54	ATGGCCTGGACCCCTCTCTGCTCCCCCTCCTCACTTTCTGCACAGTCTCTGAGGCCTCC	113		
Qy	64	TATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACACAGCGCCAGAGTACCC	123		
Db	114	TATGAGCTGACACAGCACCCCTCGGTGTCAGTGTCCCCAGGACAAAAGGCCAGAGTACCC	173		
Qy	124	TGTGGGGAGACAAACAGTAGAAATGATGTCCACTGGTACAGCAGAAAGCCAGCGCGG	183		
Db	174	TGCTCTGGAGATGCTATGCCAAAAAATATGCTTATTGTTACCAAGCAGAGTCAAGGCAG	233		

Qy	602	GCCTGACGGCCTGAGCAGTGGAAAGTCCCA	CAGAGCTACAGCTGCCAGGTACGCATGAAG	561
Db	-252	GCCTGACGGCCTGAGCAGTGGAAAGTCCCA	CAGAGCTACAGCTGCCAGGTACGCATGAAG	193
Qy	662	GGAGCACCGTGGAGAGACAGTGGGCCCTT	CACAAATGTTTCAT	703
Db	192	GGAGCACCGTGGAGAGACAGTGGGCCCTT	CACAAATGTTTCAT	151

RESULT 14

AAS87271
ID AAS87271 standard; cDNA; 791 BP.

Query Match 73.2%; Score 516; DB 23; Length 791;
Best Local Similarity 88.9%; Pred. No. 9.3e-120.

	Matches	571; Conservative	0; Mismatches	65; Indels	6; Gaps	1;
Qy	62	CCATGAAC	TGACTCAGCCAC	CCCTCGGTGTGAGTGTCC	CCAGACAGACGGCCAGATCA	121
Db	68	CCATGAGT	TGACTCAGCCAC	CCCTCAGTGTCCGTTGCC	CAGACAGACGCCAGCATCA	127
Qy	122	CCGTGGGG	GAGACACAGTGA	AAATATCTCCACTGGT	TACACAGACAGACCCAGCGC	181
Db	128	CCGTGCTT	TGGAGATAAAT	TGGGTGATAATATCTTC	GTGGTATACAGAGAGCCGGGCC	187
Qy	182	GGGCCCC	TATCTATGATG	ATGATGACCGGCCCTC	CAGGGATCCCTTGACGAT	241
Db	188	AGTCCCC	CTCTACTGGT	CTGTTACAAGATAC	CAACCGGCCCTCAGGGATCCCTTGACGAT	247
Qy	242	TCTCTGG	CTCAATCAGGG	AACACCGCACCCCTG	ACCATCAACGGGGTCGAGCCGGGG	301
Db	248	TCTCTGG	CTCAACTCTGG	AAACACAGCCACTCTG	ACCATCAACGGGCTATGG	307
Qy	302	ATCAGCG	CTGACTATTACTGT	CAGGTGTGGACAGGG	CTAGTGATCATCCGGTCTTCGGAG	361
Db	308	ATGAGGG	TGACTATTACTGT	CAGGCGTGGAC-----	AGTAACACTGTGTGCTTCGGCG	361
Qy	362	GAGGGA	CCCGGGTGACCG	CTTAGTGCAGCCCAAG	GCTGC CCCCTCGGTCACTCTGTTC	421
Db	362	GAGGGA	CCAAGCTGACCG	CTTAAGTCAGCCCAAG	GCTGC CCCCTCGGTCACTCTGTTC	421
Qy	422	CGCCCT	CTCTGAGGACTT	CAAGCCAAACAGCC	CAACTGTGTCTCTCATAGTGACT	481
Db	422	CGCCCT	CTCTGAGGAGTTC	CAAGCCAAACAGGCC	CAACTGTGTGTCTCATAGTGACT	481
Qy	482	CTTAC	CCGGGAGCCGTG	CAGTGGCCTTGAAG	GCCAGATAGACGCCCCGTCAAGCGCGGAG	541
Db	482	TCTAC	CCGGGAGCCGTG	CAGTGGCCTTGNAG	GCCAGATAGACGCCCCGTCAAGCGCGGAG	541
Qy	542	TGAGAC	CAACCA	CCCTTCAAA	CAAAAGCAACAAAGTACGGCGGCAGCGTCACTGA	601
Db	542	TGAGAC	CAACCA	CCCTTCAAA	CAAAAGCAACAAAGTACGGCGGCAGCGTATCTGA	601
Qy	602	GCCTGAC	CGCTGAGCAGT	TGGAAGTCC	CACAGAAGCTACAGCTGCCAGGTCAACGCATGAAG	661
Db	602	GCCTGAC	CGCTGAGCAGT	TGGAAGTCCA	CAGAAGCTACAGCTGCCAGGTCAACGCATGAAG	661
Qy	662	GGAGCA	CCGTGGAG	AAGACAGTGG	CCCCCTACAGAATGTTCAAT	703
Db	662	GGAGCA	CCGTGGAG	AAGACAGTGG	CCCCCTACAGAATGTTCAAT	703

RESULT 15

AAS22777
 ID AAS22777 standard; cDNA: 1825 BP.

AC AAS22777;

24-OCT-2001 (first entry)

DE Human cDNA encoding a novel human protein #343.

Human, novel protein; ss, Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cycostatic; neuroprotective; vulnery; nootropic; anticonvulsant; antithritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.

OS Homo sapiens.

XX
PN
WO200155437-A2.

02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02623.


```
PR 25-JAN-2000; 2000US-0491404.
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-451939/48.
XX P-PSDB; ANU14472.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage
XX
XX Claim 1; Page 721-722; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production..
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/ elicit an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence encodes a protein of the invention.
XX
XX Sequence 1825 BP; 361 A; 509 C; 560 G; 395 T; 0 other;
XX
Query Match 73.0%; Score 515; DB 22; Length 1825;
Best Local Similarity 87.4%; Pred. No. 2e-119;
Matches 576; Conservative 0; Mismatches 80; Indels 3; Gaps 1;
QY 45 CCCAGGTGCACGATGTCCTATGAACACTGACTCAGCCACCCTCGGTGCTCAGTGTCCTCCAGG 104
DB 73 CACAGGGCCGTGGCCCTCTATGAGCTGACTCAGCCACCCTCAGTGTCCTCCAGG 132
QY 105 ACAGAGCGCCAGGATCACTGTGGGGGAGACACAGTAGAAATGAATATGTCCACTGGTA 164
DB 133 ACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGATAAAATTGCTTGCTGTA 192
QY 165 CCAGCAGAGCCAGCGCGGCCCTTACTGTGTCATCTATGATAGTAGCAGCGCCCTC 224
DB 193 TCAGGTGAAGCCAGGCCAGTCCCTTTAGTGGTTCATCCATCAAGATACCAAGCGGCCCTC 252
QY 225 AGGGATCCCTGAGCGGATTCCTGGGTCCTCAAAATCAGGGACACGCCACCCTGACCATCA 284
DB 253 AGGGATCCCTGAGCGGATTCCTGGGTCCTCAAACTCTGGGAACACAGCCACTCTGACCATCAG 312
QY 285 CGGGGTTCAGGCGCGGGATGAGGCTGACTATTACTGTCTAGGTGTGGGACAGGGCTAGTGA 344
DB 313 CGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCTAGGCGTGGACAG---CAGCTC 369
QY 345 TCATCCGGTCTTCGGAGGAGGACCCGGGTGACCGGTCTAGGTCTAGGCCCAAGGCTGCCCC 404
DB 370 TTATGTGGCGTTTCGGCGGAGGACCAAGCTGACCGCTCTAGGTCTAGGCCCAAGGCTGCCCC 429
QY 405 CTCGGTCACTCTGTTCCTCCGCTCTCTCTGAGGAGCTTCAAGCCACAGGCCACACTGGT 464
DB 430 CTCGGTCACTCTGTTCCTCCGCTCTCTCTGAGGAGCTTCAAGCCACAGGCCACACTGGT 489
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465 GTGTCTCATAAGTGAAGTCTTCTACCCGGGAGCCCTGTGACAGTGGGCTTGAAAGGCAGATAGCAG 524
490 GTGTCTCATAAGTGAAGTCTTCTACCCGGGAGTCCGTGACAGTGGGCTTGAAAGGCAGATAGCAG 549
525 CCCCGTCAAGGCGGGAGTGGAGACACACACCCCTCCAAACAAAGCAACAAAGTACGC 584
550 CCCCGTCAAGGCGGGAGTGGAGACACACACCCCTCCAAACAAAGCAACAAAGTACGC 609
585 GGCCAGCAGCTACCTGAGCCTTGACGCTGAGCAGTGGAGAGTCCCAAGAGCTTACAGCTG 644
610 GGTGAGCAGTATCTGAGCCTGACGCTGAGCAGTGGAGAGTCCCAAGAGCTTACAGCTG 669
645 CCAGGTACGCATGAAGGAGCACCCTGGAGAGACAGTGGGCCCCCTACAGAAATGTTTCA 703
670 CCAGGTACGCATGAAGGAGCACCCTGGAGAGAGCAGTGGGCCCCCTACAGAAATATTTAT 728

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OM nucleic - nucleic search, using sw model

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Maximum Match 100%

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11: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	US-10-124-905-1	Sequence 1, Appli
2	705	100.0	705	US-09-948-429B-1	Sequence 1, Appli
3	705	100.0	705	US-10-073-138-1	Sequence 1, Appli
4	585.2	83.0	702	US-10-211-357-5	Sequence 5, Appli
5	540.2	76.6	711	US-10-124-905-9	Sequence 9, Appli
6	540.2	76.6	711	US-09-948-429B-9	Sequence 9, Appli
7	540.2	76.6	711	US-10-073-138-5	Sequence 5, Appli
8	530	75.2	868	US-09-822-849A-157	Sequence 157, App
9	512.8	72.7	960	US-09-925-301-582	Sequence 582, App
10	510.6	72.4	2667	US-10-158-646-76	Sequence 76, Appli
11	501.6	71.1	830	US-09-981-353-42	Sequence 42, Appli
12	488.6	69.3	846	US-09-981-353-55	Sequence 55, Appli
13	487	69.1	1480	US-09-981-353-146	Sequence 146, App
14	473.8	67.2	857	US-09-822-849A-158	Sequence 158, App
15	472	67.0	768	US-09-747-669-4	Sequence 4, Appli
16	472	67.0	768	US-09-747-669-5	Sequence 5, Appli
17	465.6	66.0	826	US-10-098-841-316	Sequence 316, App
18	463.2	65.7	848	US-10-158-646-70	Sequence 70, Appli
19	463	65.7	888	US-10-158-646-71	Sequence 71, Appli

ALIGNMENTS

RESULT 1

US-10-124-905-1
; Sequence 1, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,905

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Taskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 705 base pairs

20	462.8	65.6	915	10	US-09-954-456-788	Sequence 788, App
21	462.8	65.6	915	10	US-09-880-107-3743	Sequence 3743, Ap
22	461.8	65.5	883	9	US-10-158-646-73	Sequence 73, Appl
23	457.2	64.9	670	9	US-09-968-433-40	Sequence 40, Appl
24	449.2	63.7	2667	9	US-10-158-646-76	Sequence 76, Appl
25	447.6	63.5	2112	9	US-10-001-857-108	Sequence 108, App
26	435.6	61.8	885	9	US-09-852-797-47	Sequence 47, Appl
27	435.6	61.8	885	10	US-09-853-161-47	Sequence 47, Appl
28	435.6	61.8	885	10	US-09-852-659A-47	Sequence 47, Appl
29	434	61.6	879	9	US-09-852-797-29	Sequence 29, Appl
30	434	61.6	879	10	US-09-853-161-29	Sequence 29, Appl
31	434	61.6	879	10	US-09-852-659A-29	Sequence 29, Appl
32	432.2	61.3	928	9	US-09-852-797-46	Sequence 46, Appl
33	432.2	61.3	928	10	US-09-853-161-46	Sequence 46, Appl
34	432.2	61.3	928	10	US-09-852-659A-46	Sequence 46, Appl
35	415.4	58.9	1480	9	US-09-981-353-146	Sequence 146, Appl
36	407.4	57.8	579	9	US-10-158-646-75	Sequence 75, Appl
37	395.4	56.1	764	9	US-09-981-353-46	Sequence 46, Appl
38	392.4	55.7	491	9	US-09-736-457-833	Sequence 833, App
39	392.4	55.7	491	9	US-09-902-941-833	Sequence 833, App
40	392.4	55.7	491	9	US-09-849-626-833	Sequence 833, App
41	392.4	55.7	491	9	US-10-017-754-833	Sequence 833, App
42	389.4	55.2	558	9	US-09-920-455-58	Sequence 58, Appl
43	387.4	55.0	608	9	US-09-736-457-908	Sequence 908, App
44	387.4	55.0	608	9	US-09-902-941-908	Sequence 908, App
45	387.4	55.0	608	9	US-09-849-626-908	Sequence 908, App

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: lambda variable and constant domains in
CE9.1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..702
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..702
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-211-357-5
Query Match 83.0%; Score 585.2; DB 9; Length 702;
Best Local Similarity 89.6%; Pred. No. 2.3e-168;
Matches 629; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 4 AGGGTCCCGCTCAGCTCCTGGGGCTCTGCTCTGCTCCAGGTGCACGATGTGC 63
DB 1 ATGGCTGGGCTCTGCTCTCTCGGCTCTGCTCACTTTACAGACTCTGGGCTCC 60
QY 64 TATGAAGTACTAGCTCAGCCACCTCGGTGTAGTGTCCCGAGGACAGCGGCAGGATCAC 123
DB 61 TATGAGTTGAGTCAGCTCAGTGTCTGCTCCAGGACAGACGCGCGGTTTCA 120
QY 124 TGTGGGGGACACAGTAAATATGTCTCACTGTGTACAGGATCCCTGAGCGATTC 183
DB 121 TGTGGGGGACACAGTGTGAAGAAAGTGTACAGTGTGTACAGAGGACCGCCAG 180
QY 184 GCCCTATATCTGCTATCTATGATGATGACGCGGCTCTGAGGATCCCTGAGCGATTC 243
DB 181 GCCCTGTGCTGCTATCTATGCTGACAGGACGCGCTCAGGATCCCTGCGGATTC 240
QY 244 TCTGGCTCCAAATCAGGGAACACCGCACCTGACCATCAACCGGGTTCAGGCGCGGAT 303
DB 241 TCTGGCTCCAAATCAGGGAACACCGCACCTGACCATCAACCGGGTTCAGGCGCGGAT 300
QY 304 GAGGCTGACTATTACTGTAGGTGTGGACAGGGCTAGTATCATCGGTCTTCGAGGA 363
DB 301 GAGGCTGACTATTACTGTAGGTGTGGACAGGCTAGTATCATCGGTCTTCGAGGA 360

QY 364 GGGACCCGGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC 423
DB 361 GGGACCCGGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC 420
QY 424 CCCTCTCTGAGGAGCTTCAAGCCCAAGGCACTGGTGTGTCTCTAAGTCACTTC 483
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QY 484 TACCCGGGAGCGGTGACAGTGGCCCTGGAAGGAGATAGCAGCCCGTCAAGCGGAGTG 543
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QY 544 GAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCGAGGCTACCTGAGC 603
DB 541 GAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCGAGGCTACCTGAGC 600
QY 604 CTGAGCGCTGAGCAGTGGAGTCCCAAGAGTACAGCTGCGAGTACGCGATGAGGG 663
DB 601 CTGAGCGCTGAGCAGTGGAGTCCCAAGAGTACAGCTGCGAGTACGCGATGAGGG 660
QY 664 AGCACCGTGGAGAGACAGTGGCCCTACAGATGTTATGA 705
DB 661 AGCACCGTGGAGAGACAGTGGCCCTACAGATGTTATGA 702
RESULT 5
US-10-124-905-9
Sequence 9, Application US/10124905
Patent No. US20020166136A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: CDS
LOCATION: 1..711
NAME/KEY: mat_peptide
LOCATION: 1..711
US-10-124-905-9

Query Match 76.6%; Score 540.2; DB 9; Length 711;

Best Local Similarity 86.1%; Pred. No. 1.1e-154;
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGGTCCCGCTCAGCTCTGGGCTCTGCTCTGGCTCCAGGTGACCATGT 60
DB 1 ATGAGGGTCCCGCTCAGCTCTGGGCTCTGCTCTGGCTCCAGGTGACCATGT 60
QY 61 GCCTATGAATGACTCAGCCACCTCGGTGTAGTGTCCCGAGGAGGAGGAGG 120
DB 61 GAGTCTGTCTGACACAGCGGCTCAGTGTCTGGGCTCCAGGAGGAGGAGG 120
QY 121 ACTGTGGGGG-----AGACAACAGTAGAATATGATGATGATGATGATG 174
DB 121 TGTGCTGCTGACACAGCGGCTCAGTGTCTGGGCTCCAGGAGGAGGAGG 180
QY 175 CCAGCGGGGCTCTACTGCTCAGTGTATGATGATGATGATGATGATGATG 234
DB 181 CCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 235 GAGCGATTCTCTGGCTCCAAATCAGGAGGAGGAGGAGGAGGAGGAGGAGG 294
DB 241 GAGCGATTCTCTGGCTCCAAATCAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 295 GCGGGGATGAGCTGACTATTAATGATGATGATGATGATGATGATGATGATG 354
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DB 361 TTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
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QY 475 AGTGAATTTACCGGGAGCGGTGACAGTGGCTGGAAGGAGGAGGAGGAGGAGG 534
DB 481 AGTGAATTTACCGGGAGCGGTGACAGTGGCTGGAAGGAGGAGGAGGAGGAGG 540
QY 535 GCGGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 594
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QY 595 TACCTGAGCTGACGCTGAGCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 654
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DB 661 CATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 711

RESULT 6

US-09-948-429B-9

Sequence 9, Application US/09948429B

Patent No. US20020177689A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONOCLONAL ANTIBODIES SPECIFIC

TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 711 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: CDS

LOCATION: 1..711

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 1..711

US-09-948-429B-9

Query Match

Best Local Similarity 76.6%; Score 540.2; DB 9; Length 711;

Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGGTCCCGCTCAGCTCTGGGCTCTGCTCTGGCTCCAGGTGACCATGT 60

DB 1 ATGAGGGTCCCGCTCAGCTCTGGGCTCTGCTCTGGCTCCAGGTGACCATGT 60

QY 61 GCCTATGAATGACTCAGCCACCTCGGTGTAGTGTCCCGAGGAGGAGGAGG 120

DB 61 GAGTCTGTCTGACACAGCGGCTCAGTGTCTGGGCTCCAGGAGGAGGAGG 120

QY 121 ACTGTGGGGG-----AGACAACAGTAGAATATGATGATGATGATGATG 174

DB 121 TGTGCTGCTGACACAGCGGCTCAGTGTCTGGGCTCCAGGAGGAGGAGG 180

QY 175 CCAGCGGGGCTCTACTGCTCAGTGTATGATGATGATGATGATGATGATGATG 234

DB 181 CCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

QY 235 GAGCGATTCTCTGGCTCCAAATCAGGAGGAGGAGGAGGAGGAGGAGGAGG 294

DB 241 GAGCGATTCTCTGGCTCCAAATCAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

QY 295 GCGGGGATGAGCTGACTATTAATGATGATGATGATGATGATGATGATGATG 354

DB 301 ACTGAGGATGAGCTGACTATTAATGATGATGATGATGATGATGATGATGATG 360

QY 355 TTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 414

DB 361 TTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

QY 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACACTGGTGTCTCATA 474
Db 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACACTGGTGTCTCATA 480
QY 475 AGTGACTTCTACCGGGGCGGTGACAGTGGCTTGAAGCCAGATAGCAGCCCGTCAAG 534
Db 481 AGTGACTTCTACCGGGGCGGTGACAGTGGCTTGAAGCCAGATAGCAGCCCGTCAAG 540
QY 535 GCGGGAGTGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 594
Db 541 GCGGGAGTGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
QY 595 TACCTGAGCTGAGCGCTGAGCTGAGTGAAGTCCACAGAGCTACAGTGCACAGGTCACG 654
Db 601 TACCTGAGCTGAGCGCTGAGCTGAGTGAAGTCCACAGAGCTACAGTGCACAGGTCACG 660
QY 655 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705
Db 661 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711

RESULT 7

US-10-073-138-5
; Sequence 5, Application US/10073138
; Publication No. US20020187146A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabil
; BRAMS, Peter

TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
AND B7.2 CO-STIMULATORY ANTIGENS

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 1..711
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-073-138-5

Query Match 76.6%; Score 540.2; DB 9; Length 711;
Best Local Similarity 86.1%; Pred. No. 1.1e-154;
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;
QY 1 ATGAGGATCCCGCTCAGCTCCTGGGGCTCTGCTGCTCTGGCTCCAGGTCCAGGTCACGATCT 60
Db 1 ATGAGGATCCCGCTCAGCTCCTGGGGCTCTGCTGCTCTGGCTCCAGGTCCAGGTCACGATCT 60
QY 61 GCCTATGAATCACTCAGCCACCTCGGTGTCCAGTGTCCAGGACAGACGCGCCAGGATC 120
Db 61 GAGTCTGTCTGACACAGCGGCCCTCAGTGTCTGGGGCCCGCAGGACAGAGGTCCACATC 120
QY 121 ACCTGTGGGG-----AGACAAACAGTAGAATATGTCCACTGGTACACAGAGAAG 174
Db 121 TCGTGACCTGGGAGCAGCTCCAAACATTGGAGGTATGATCTATCTATGGTACCAGCAGCTC 180
QY 175 CAGCGCGGGGCCCTATCTATGTGTATCTATGTAGTAGCGGCGCTCAGGATCCCT 234
Db 181 CCAGGAACGGGCCCCCAAACTCCTCATATGACATTAAACAAGCAGCCCTCAGGAATTTCT 240
QY 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCACCTCACCATCAACGGGGTCGAG 294
Db 241 GACCGATTCTCTGGCTCCAAAGTCTGTACCGCGGCTCCTCTGGCCATCTACTGGGCTCCAG 300
QY 295 GCGGGGATGAGGCTGACTTATTCTGTCTGAGGTGTGGGACAGGGCTAGTGATCATCCGGTC 354
Db 301 ACTGAGGATGAGGCTGATTATTCTGCGCAGTCTTATGACAGCAGCCTGAATGCTCAGGTA 360
QY 355 TTGCGAGGAGGACCGCGGTGACCGTCTAGTGTAGCCCAAGGTGCCCCCTCGGTCACT 414
Db 361 TTGCGAGGAGGACCGCGGTGACCGTCTAGTGTAGCCCAAGGTGCCCCCTCGGTCACT 420
QY 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACACTGGTGTCTCATA 474
Db 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAGGCCACACACTGGTGTCTCATA 480
QY 475 AGTGACTTCTACCGGGGCGGTGACAGTGGCTTGAAGCCAGATAGCAGCCCGTCAAG 534
Db 481 AGTGACTTCTACCGGGGCGGTGACAGTGGCTTGAAGCCAGATAGCAGCCCGTCAAG 540
QY 535 GCGGGAGTGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 594
Db 541 GCGGGAGTGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
QY 595 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCACAGGTCACG 654
Db 601 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCACAGGTCACG 660
QY 655 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705
Db 661 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711

RESULT 8

US-09-822-849A-157
; Sequence 157, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakr
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582

; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 832
; OTHER INFORMATION: n = a,c,t, or g
US-09-822-849A-157

Query Match 75.2%; Score 530; DB 10; Length 868;
Best Local Similarity 89.1%; Pred. No. 1.5e-151;
Matches 572; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 62 CCTATCACTGACTAGCCACCTCGGTGTCAGTGTCCCGAGGACAGCGCCAGGATCA 121
DB 86 CCTATGTCGTGACGCGACACCTCGGTGTCAGTGTCCCGAGGACAGCGCCAGGATCA 145
QY 122 CTTGTGGGGGAGACAACTAGATAATGATATGTCACCTGCTACCAAGAGAGAGAGAGAG 181
DB 146 CGTGTGTGGGACAGCATGTTGGAGTAAAGTGTGAAGTGTGATCAAGAGAGAGAGAG 205
QY 182 GGGCCCTTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
DB 206 AGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265
QY 242 TCTTCTGCTTCCAAATCAGGAGACACCGCCACCTGACCATCAACGGGGTTCAGGGCGGG 301
DB 266 TCTTCTGCTTCCAACTCTGAAACACCGCCACCTGACCATCAACGGGGTTCAGGGCGGG 325
QY 302 ATGAGGCTCACTATTACTGTGAGTGTGGAGAGGCTAGTATCATCGGCTTCGCGAG 361
DB 326 ATGAGGCGCACTATTATGTCACCTTGGTTTATCAAGTGTGAGGCGGTTTCGCGG 385
QY 362 GAGGAGCCGGGTGACCGTCTAGGTGACGCCAAGGCTGCCCTCGGTCACTCTGTTC 421
DB 386 GAGGAGCAAGCTGACCGCTACGTGACGCCAAGGCTGCCCTCGGTCACTCTGTTC 445
QY 422 CGCCCTCTCTGAGGAGCTTCAAGCAACAGGCACTGCTGTCTCATAGTGACT 481
DB 446 CGCCCTCTCTGAGGAGCTTCAAGCAACAGGCACTGCTGTCTCATAGTGACT 505
QY 482 TCTACCCGGGAGCCGTGACGTGGCTGGAAGGACATAGCAGCCCGTCAAGGGCGGAG 541
DB 506 TCTACCCGGGAGCCGTGACGTGGCTGGAAGGACATAGCAGCCCGTCAAGGGCGGAG 565
QY 542 TGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCGCAGCAGCTACTGA 601
DB 566 TGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCGCAGCAGCTACTGA 625
QY 602 GCTGTAGCGCTGAGCAGTGGAGTCCCAAGAGTACAGTGTCCAGGTCAGCGATGAAG 661
DB 626 GCTGTAGCGCTGAGCAGTGGAGTCCCAAGAGTACAGTGTCCAGGTCAGCGATGAAG 685
QY 662 GGAGCACCTGTGAGAGAGAGTGGCCCTTACAGATGTTTCAT 703
DB 686 GGAGCACCTGTGAGAGAGAGTGGCCCTTACAGATGTTTCAT 727

RESULT 9
US-09-925-301-582
; Sequence 582, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882

; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 582
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (924)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (937)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (939)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-582

Query Match 72.7%; Score 512.8; DB 10; Length 960;
Best Local Similarity 82.4%; Pred. No. 2.6e-146;
Matches 577; Conservative 8; Mismatches 115; Indels 0; Gaps 0;
QY 4 AGGGTCCCGCTCAGCTCCTCGGGGCTCTGCTGCTTGGCTCCCAAGGTGCACGATGTGC 63
DB 34 ATGGGCTGGACCCCTCTCTGCTGCTCCCTCTCTCTCTGTCACAGTCTCTGAGGCTCC 93
QY 64 TATGAATGACTCAGCCACCTCGGTGTCAGTGTCCCGAGGACAGAGCCAGGATCACC 123
DB 94 TATGAGTGCACAGCCACCTCGGTGTCAGTGTCCCGAGGACAAACCGCCMGGATCACC 153
QY 124 TGTGGGGAGACAAACAGTAGAATGAATATGTCCTGCTGACAGAGAGCCAGCGCG 183
DB 154 TGCTCTGAGATGCTGTTGCCAATAAATAATCTTATTGTGACAGAGAGTTCAGGCCAG 213
QY 184 GCCCTTATCTGCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
DB 214 GCCCTTGTGTGCTCATCTATGAGGACACAGACGACCTCTCGCGATCTCTGAGAGATTC 273
QY 244 TCTGGCTCAAAATCAGGAGACACCGCCACCTGACCATCAACGGGGTTCAGGGCGGGGAT 303
DB 274 TCTGGCTCCAGCTCAGGAGCAATGGCCACTTTGACTATCATGTTGGGGCCCGAGGAT 333
QY 304 GAGGCTGACTATTACTGTGAGGTGAGGACAGGCTAGTATCATCCGGTCTTCGAGAG 363
DB 334 GAAGCGGACTACTACTGCTACTCAACAGACAGCAGTCTTATTACAGGGTGTTCGGCGGA 393
QY 364 GGGACCCGGGTGACCGTCTCTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTCCCG 423
DB 394 GGGACCAAGTCAACCGTCTCTAGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTTCCCG 453
QY 424 CCCTCTCTGAGAGGCTTCAAGCCCAAGAGGCAACACTGGTGTGTCATAGTACTTTC 483
DB 454 CCCTCTCTGAGAGGCTTCAAGCCCAAGAGGCAACACTGGTGTGTCATAGTACTTTC 513
QY 484 TACCCGGGAGCGCTGACAGTGGCTTGGAGGAGCAGATAGCAGCCCGTCAAGGGCGGAGTG 543
DB 514 TACCCGGGAGCGCTGACAGTGGCTTGGAGGAGCAGATAGCAGCCCGTCAAGGGCGGAGTG 573
QY 544 GAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCGCAGCAGTACCTGAGC 603
DB 574 GAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCGCAGCAGTACCTGAGC 633
QY 604 CTGAGCCTGAGCAGTGGAGTCCCAAGAGTCCCAAGAGTCCAGGTCAGGATGAGAGGG 663
DB 634 CTGAGCCTGAGCAGTGGAGTCCCAAGAGTCCCAAGAGTCCAGGTCAGGATGAGAGGG 693
QY 664 AGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCAT 703
DB 694 AGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCAT 733

RESULT 14
US-09-822-849A-158
; Sequence 158, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 158
; LENGTH: 857
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-158

Query Match 67.2%; Score 473.8; DB 10; Length 857;
Best Local Similarity 83.3%; Pred. No. 1.9e-134;
Matches 554; Conservative 0; Mismatches 102; Indels 9; Gaps 1;

QY 48 AGCTGACGATGTCCTATGAATGACTCAGCCACCTCGGTCTCAGTGTCCCGACGACA 107
DB 54 AGTTCTGTGGTTCTTCTGAGCTGACTCAGGACCTGTGTGTGTGGCCCTGGGACA 113
QY 108 GACGGCCAGGATCACCTGTGGGGAGACACAGTAGAAATGAATATGTCACCTGGTACCA 167
DB 114 GACAGTCAGGATCACATGCCGAGGAGACACCTCGGAAAGTATTATACAAATTTGGTACCA 173
QY 168 GCAGAGCCAGCGGGGCCCTTACTGTGTATCTATGATGATA-----GTACCG 218
DB 174 ACTGAAGCCAGGACAGGCCCTCTCTGTGTGATGTTGTAATAAACAACCGGACACCG 233
QY 219 GCCTCAGGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGAACACCGCCACCTGTAC 278
DB 234 GCCCTCAGGAATCCCAAGACGATCTCTGGCTCCACTTCAGGAACACAGCTTCCCTTGAC 293
QY 279 CATCAACGGGGTCGAGCGGGGATGAGGCTGACTATTACTGTGAGTGTGGACAGGGC 338
DB 294 CATCACTGGGGCTCAGGTTGAAGTNGTCTGACTTTTACTGTAGTTCCCGGACAGCAG 353
QY 339 TAGTGATCATCCGGTCTTTCGGAGAGGACCCCGGTGACCGTCTTAGGTGAGCCCAAGGC 398
DB 354 TGGTAAAAATTGGGTGTTTCGGCGGTGGGACCAAGCTGACCGTCTTAAGTCAGCCCAAGGC 413
QY 399 TGCCCCCTCGTCACTCTGTTCCGGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCAC 458
DB 414 TGCCCCCTCGTCACTCTGTTTCCACCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCAC 473
QY 459 ACTGGTGTGTCTCATAGTGAATTTCTACCCGGGAGCGGTGACAGTGGCCCTGGAAGGCAGA 518
DB 474 ACTGGTGTGTCTCATAGTGAATTTCTACCCGGGAGCGGTGACAGTGGCCCTGGAAGGCAGA 533
QY 519 TAGCAGCCCGTCAAGCGGAGTGTGAGACCAACACACCTTCCAAACAAAGCAACACAA 578
DB 534 TAGCAGCCCGTCAAGCGGAGTGTGAGACCAACACACCTTCCAAACAAAGCAACACAA 593
QY 579 GTACGGGGCAGCAGTACCTGAGCCTGAGCCTGAGCAGTGAAGTCCCAAGAGCTA 638
DB 594 GTACGGGGCAGCAGTACCTGAGCCTGAGCCTGAGCAGTGAAGTCCCAAGAGCTA 653

QY 639 CAGCTGCCAGGTCACGCATGAAGGGAGCACCTGGAGAGACAGTGGCCCTTACAGAATG 698
DB 654 CAGCTGCCAGGTCACGCATGAAGGGAGCACCTGGAGAGACAGTGGCCCTTACAGAATG 713
QY 699 TTTCAT 703
DB 714 TTTCAT 718

RESULT 15
US-09-747-669-4
; Sequence 4, Application US/09747669
; Patent No. US20020122807A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-747-669-4

Query Match 67.0%; Score 472; DB 10; Length 768;
Best Local Similarity 84.4%; Pred. No. 6.5e-134;
Matches 545; Conservative 0; Mismatches 95; Indels 6; Gaps 1;

QY 64 TATGAACGTACCTCAGCCACCTCGGTGTGTCAGTGTCCCGGAGGACAGCGCCAGGATCACC 123
DB 79 TCTGTCTGACTCAGCCACCTCAGCGTCTGGACCCCGGAGGAGGTTCACCAITCTCT 138
QY 124 TGTGGGGGAGACAACAGTA-----GAAATGAATATGTCCACTGTGTACAGAGAGCA 177
DB 139 TGTCTTGAAGCACTCCAAATCGAAGTAAGACTGTAACTGTGTACCAAGCACTCCCA 198
QY 178 GCGGGGGCCCTTATCTGTGTCTATGTATGTAGTAGTACCGGCGCTCAGGGATTCCTGAG 237
DB 199 GGAACGGGGCCCAAAATTTCTCATCTATAGTAATAATCAGCGGCCCTCAGGGGTCCCTGAC 258
QY 238 CGATTTCTGTGGTCCAAATCAGGGAACACCGCCACCTGACCATCAACCGGGTCCAGGGCC 297
DB 259 CGATTTCTGTGGTCCAAAGTCTGGCACCTCAGCGCTCCCTGGCCATCAGTGGGTCCAGTCT 318
QY 298 GGGGATGAGCGCTGACTATTACTGTGAGGTGGGACAGGGCTAGTGTATCATCCGGTCTTC 357
DB 319 GAGGATGAGCGTGAATTTACTGTGCAGCATGGGATGACAGCTGAATGGTGGGTGTTTC 378
QY 358 GGAGGAGGACCCGGGTGACCGTCTCTAGGTGACGCCCAAGGCTGCCCTCGGTCACTCTG 417
DB 379 GCGGAGGAGCAAAAGCTGACCGTCTCTGGGTGACGCCCAAGGCTGCCCTCGGTCACTCTG 438
QY 418 TTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACACTGGTGTCTCATAGT 477
DB 439 TTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACACTGGTGTCTCATAGT 498
QY 478 GACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGAGATAGAGAGCCCGGTCAAGGCG 537
DB 499 GACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGAGATAGAGAGCCCGGTCAAGGCG 558
QY 538 GGAGTGGAGACCAACCAACCCCTCCAAACAAAGCAACAGTACGCGGCCAGAGCTAC 597

Db	559	GGAGTGGAGACCAACACCCCTCCAAACAAAGCAACAAGTACCGGGCCAGCTAC	618
Qy	598	CTGAGCCTGACGCTGAGCAGTGGAAAGTCCACAGAAGCTTACAGCTGCCAGGTCAAGCAT	657
Db	619	CTGAGCCTGACGCTGAGCAGTGGAAAGTCCACAGAAGCTTACAGCTGCCAGGTCAAGCAT	678
Qy	658	GAAGGGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAATGTTTCAT	703
Db	679	GAAGGGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAATGTTTCAT	724

Search completed: June 3, 2003, 23:03:33
Job time : 95.9453 secs

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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:26:38 ; Search time 40.2104 Seconds
(without alignments)
5376.898 Million cell updates/sec

Title: US-09-576-424-1
Perfect score: 705
Sequence: 1 atgagggtcccgctcagct.....ccccacagaatgttcata 705

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	3	US-08-487-550-1
2	585.2	83.0	702	3	US-08-523-894-5
3	540.2	76.6	711	3	US-08-487-550-9
4	473	67.1	935	3	US-09-049-672A-20
5	457	64.8	902	2	US-08-378-939-11
6	456	64.7	895	3	US-09-049-672A-25
7	455.4	64.6	891	3	US-09-049-672A-23
8	435.6	61.8	885	4	US-09-152-060-47
9	434	61.6	879	4	US-09-152-060-29
10	432.2	61.3	928	4	US-09-152-060-46
11	425.4	60.3	916	3	US-09-049-672A-24
12	407.4	57.8	716	4	US-08-793-450-5
13	306.6	43.5	584	4	US-09-404-879A-268
14	273.2	38.8	771	4	US-08-991-789A-241
15	273.2	38.8	771	4	US-09-062-451-241
16	273.2	38.8	771	4	US-09-598-326-241
17	267.2	37.9	387	1	US-08-379-072A-20
18	267.2	37.9	387	1	US-08-478-039-109
19	267.2	37.9	387	1	US-08-481-869-20
20	267.2	37.9	387	1	US-08-476-349A-109
21	267.2	37.9	387	1	US-08-476-237-16
22	267.2	37.9	387	3	US-08-523-894-3
23	260.4	36.9	327	4	US-09-202-181-1
24	259.4	36.8	408	4	US-09-025-769B-169
25	249.8	35.4	642	2	US-08-634-783A-4
26	249.8	35.4	642	3	US-09-070-817-4
27	246.2	34.9	346	2	US-08-761-277A-50

Query Match 100.0% ; Score 705 ; DB 3 ; Length 705 ;

28	246	34.9	333	2	US-08-477-553A-44	Sequence 44, Appl
29	244.2	34.6	324	1	US-08-259-372A-9	Sequence 9, Appl
30	244.2	34.6	324	1	US-08-468-671-9	Sequence 9, Appl
31	242.4	34.4	318	2	US-08-646-981-4	Sequence 4, Appl
32	237.4	33.7	431	2	US-08-345-321-7	Sequence 7, Appl
33	226.4	32.1	318	1	US-08-436-463-9	Sequence 9, Appl
34	226.4	32.1	318	1	US-08-024-253-9	Sequence 9, Appl
35	212	30.1	324	1	US-08-360-123-10	Sequence 10, Appl
36	212	30.1	324	2	US-08-450-578-10	Sequence 10, Appl
37	212	30.1	324	2	US-09-017-628-10	Sequence 10, Appl
38	212	30.1	324	2	US-09-014-880-10	Sequence 10, Appl
39	212	30.1	324	4	US-08-450-363-10	Sequence 10, Appl
40	202.2	28.7	314	4	US-09-370-838-13	Sequence 13, Appl
41	200.2	28.4	831	4	US-09-260-527-2	Sequence 2, Appl
42	200.2	28.4	840	4	US-09-260-527-4	Sequence 4, Appl
43	199.4	28.3	930	4	US-09-079-029-6	Sequence 6, Appl
44	199.4	28.3	939	4	US-09-079-029-7	Sequence 7, Appl
45	187.6	26.6	318	1	US-08-259-372A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-1
; Sequence 1, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 1..705
US-08-487-550-1

QY 544 GAGACACACACCCCTCCAAACAAAGCAACAAAGTACGGCCGACGAGCTACCTGAGC 603
DB 541 GAGACACACACACCCCTCCAAACAAAGCAACAAAGTACGGCCGACGAGCTACCTGAGC 600
QY 604 CTGACCCCTGAGCAGTGGAGTCCCAACAGAGCTACAGCTGCCAGGTACGATGAAGG 663
DB 601 CTGACCCCTGAGCAGTGGAGTCCCAACAGAGCTACAGCTGCCAGGTACGATGAAGG 660
QY 664 AGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705
DB 661 AGCACCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 702

RESULT 3
US-08-487-550-9
; Sequence 9, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..711
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 1..711
US-08-487-550-9

Query Match 76.6%; Score 540.2; DB 3; Length 711;
Best Local Similarity 86.1%; Pred. No. 1.5e-140;
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGTCCTCCCTCAGCTCTGGGCTCTCTGCTCTGGTCCAGTGCACCATGT 60
DB 1 ATGAGGTCCTCCCTCAGCTCTGGGCTCTCTGCTCTGGTCCAGTGCACCATGT 60
QY 61 GCCTATGACTGACTCAGCCACCTCTGGTGTAGTGTCCCTCAGAGACAGCGGCAGATC 120
DB 61 GAGTCTGTCTGACAGCGCCCTCTAGTGTCTGGGGCCCCCAGGAGAGGTCAACATC 120

QY 121 ACCTGTGGGG-----AGACAAACAGTAGAAATGATATGTCCACTGGTACGAGAGAAG 174
DB 121 TCGTGCACTGGGAGCAGCCTCCAAACATTGGAGGTATGATCTACTATTGGTACCAGCAGCTC 180
QY 175 CCAGCGGGGGCCCTTACTGTCTATGATGATGATGACCGGCCCTCAGGGATCCCT 234
DB 181 CCAGGAACGGGGCCCCAACTCTCTATGACATTTAAACAGCGACCCCTCAGGAATTTCT 240
QY 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACCGGGGTCGAG 294
DB 241 GACCGATTCTCTGGCTCCAAATCTGGTACCGGGCTCTCTGGCCATCATCTGGGCTCCAG 300
QY 295 GCCGGGATGAGGCTGACTATTACTGTCTAGGTGTGGGACAGGGCTAGTGTATCATCCGGTC 354
DB 301 ACTGAGGATGAGGCTGATTATTACTTGCAGTCTCTATGACAGCAGCGCTGAATGCTCAGGTA 360
QY 355 TTGGGAGGAGGACCGGGTGACCGTCTAGGTGACGCCCAAGGCTGCCCTCGGTCACT 414
DB 361 TTGGGAGGAGGACCGGGTGACCGTCTAGGTGACGCCCAAGGCTGCCCTCGGTCACT 420
QY 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAGGCCACACTGGTGTCTCATA 474
DB 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAGGCCACACTGGTGTCTCATA 480
QY 475 ACTGACTTCTACCGGGAGCCGTGACAGTGGCTGGAAGGAGATAGCAGCCCGTCAAG 534
DB 481 AGTGACTTCTACCGGGAGCCGTGACAGTGGCTGGAAGGAGATAGCAGCCCGTCAAG 540
QY 535 GCGGAGTGGAGACCAACACACCTCTCAACAAAGCAACAAAGTACCGGGCCAGC 594
DB 541 GCGGAGTGGAGACCAACACACCTCTCAACAAAGCAACAAAGTACCGGGCCAGC 600
QY 595 TACCTGAGCTGACCGCTGACAGTGGAGTCCACAGAACTTACAGTGCAGGTCACG 654
DB 601 TACCTGAGCTGACCGCTGACAGTGGAGTCCACAGAACTTACAGTGCAGGTCACG 660
QY 655 CATGAAGGAGCAGCCGTGGAGAGACAGTGGCGCCCTTACAGAATGTTTCATGA 705
DB 661 CATGAAGGAGCAGCCGTGGAGAGACAGTGGCGCCCTTACAGAATGTTTCATGA 711

RESULT 4
US-09-049-672A-20
; Sequence 20, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536

APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Cuxley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THYRN0110
CLONE: 2872705
US-09-049-672A-23

Query Match 64.8%; Score 455.4; DB 3; Length 891;
Best Local Similarity 79.8%; Pred. No. 4.9e-117;
Matches 566; Conservative 0; Mismatches 131; Indels 12; Gaps 2;

QY 4 AGGGTCCCGCTCAGCTCCCTGGGCTCTGCTGCTCCAGGTCCAGGTGCACGATGTGC 63
DB 34 ATGGCTGGGCTGTGTTATTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 93
QY 64 TATGAATGACTCAGCCACCTCGGTGTAGTGTCTCCAGGACAGCGCCAGGATCACC 123
DB 94 TCTGCCCTGACTCAGCTGCTCGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 153
QY 124 TGTGGGGGAGAACACAGTA-----GAAATGATATGCTCCACTGGTACGACGAGAAG 174
DB 154 TGCACGTGAACACGACGATGACGTGTGGTGTATTAATGCTCTCTGGTACCAACAGTCC 213
QY 175 CCAGCGCGGCGCCCTTACTGCTCATCTATGATGATGATGACCGCGCCCTCAGGGATCCCT 234
DB 214 CCAGGACGCGCGCCCAACTCATGTTATGAGTGTGATGATGATGATGATGATGATGATGAT 273
QY 235 GAGCGATTCTGTGGTCCAAATCAGGGAACACCGCCACCTGTACCATCAACCGGGTCGAG 294
DB 274 AATCGGTTCTGTGGTCCAAATCAGGGAACACCGCCACCTGTACCATCAACCGGGTCGAG 333
QY 295 GCGGGGATGAGCTGACTTATTACTGTGAGTGTGGGACAGGCTAGTATCATCGGTC 354
DB 334 GCTGAGGACGAGGCTGATTATTACTG---CAGCTCATATGTAGGCAACAACTTGTGGTA 390

QY 355 TTCGAGGAGGAGGACCCGGGTGACCGTCTAGTTCAGCCCAAGGCTGCCCCCTCGGTCACT 414
DB 391 TTCGCGGAGGAGGACCAAGCTGACCGTCTAGTTCAGCCCAAGGCTGCCCCCTCGGTCACT 450
QY 415 CTGTTCCCGCCCTCTCTCTGAGGAGCTTCAAGCAACAGGCGCCACACTGGTGTCTCATA 474
DB 451 CTGTTCCCGCCCTCTCTCTGAGGAGCTTCAAGCAACAGGCGCCACACTGGTGTCTCATA 510
QY 475 AGTGACTTCTACCCGCGGAGCGGTGACAGTGGCTGGAAGGAGATAGACGCGCCGTCAG 534
DB 511 AGTGACTTCTACCCGCGGAGCGGTGACAGTGGCTGGAAGGAGATAGACGCGCCGTCAG 570
QY 535 GCGGAGTGGAGACCAACCAACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 594
DB 571 GCGGAGTGGAGACCAACCAACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 630
QY 595 TACCTGAGCTGACGCTGAGCAGTGGAGTGGAGTCCCAAGAGTACAGTGCAGGTCACG 654
DB 631 TATCTGAGCTGACGCTGAGCAGTGGAGTGGAGTCCCAAGAGTACAGTGCAGGTCACG 690
QY 655 CATGAGGAGGACCGGTGGAGAGACAGTGGCGCCCTACAGATGTTTCAT 703
DB 691 CATGAGGAGGACCGGTGGAGAGACAGTGGCGCCCTACAGATGTTTCAT 739

RESULT 8

US-09-152-060-47
Sequence 47, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1 US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47
LENGTH: 885
TYPE: DNA
ORGANISM: Homo sapiens
US-09-152-060-47

Query Match 61.8%; Score 435.6; DB 4; Length 885;
Best Local Similarity 81.2%; Pred. No. 1.5e-111;
Matches 520; Conservative 0; Mismatches 114; Indels 6; Gaps 1;

QY 70 CTGACTCAGCCACCTCGGTGTGCTGCTCCAGGACAGCGCCAGGATCAGCTGTGG 129
DB 87 CTGACTCAGCCACCTCGGTGTGCTGCTCCAGGACAGCGCCAGGATCAGCTGTGG 146
QY 130 GGAGACAACAGTGAAGATG-----AATATGTCCACTGGTACCAGAGACCGCGCG 183

Db 147 GGGAAACAACAAATGTTGGCGACCAAGGAGCAGCTTGGCTGCAGCAGCACACAGGCCAC 206
QY 184 GCCCTTATCTGCTCATCTATGATGATAGTAGACCGGCCCTCAGGGATCCCTCAGCGATTTC 243
Db 207 CTTCCCAAACTCTGCTCTACAGGAATAAFAACCGGCCCTCAGGGATCTCAGAGATTTC 266
QY 244 TCTGGCTCCAAATCAGGGAACACCGCACCTGACCATCAACCGGGTCAGGCGCGGGAT 303
Db 267 TCTGCATCCAGGTCAGGAGCCACATCTCCCTGACCAATTAAGTCTCAGAGCTGAGGAC 326
QY 304 GAGCGTGACTATTACTGTCAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363
Db 327 GAGCGTGACTATTACTGTCGAGCAGATATGACAGCAGCTTCAGTTTGGATGTTTCGGCGGA 386
QY 364 GGACCGGGGTGACCGCTCTAGTGCAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCG 423
Db 387 GGGACCAAGCTGACCGCTCTAGTGCAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCA 446
QY 424 CCTCTCTGAGAGCTTCAAGCAACAAGGCGACACTGGTGTCTCATAGTGACTTC 483
Db 447 CCTCTCTGAGAGCTTCAAGCAACAAGGCGACACTGGTGTCTCATAGTGACTTC 506
QY 484 TACCGGGAGCGCTGACAGTGGCTGGAAGGCGAGTAGCAGCCCGCTCAAGGCGGAGTG 543
Db 507 TACCGGGAGCGCTGACAGTGGCTGGAAGGCGAGTAGCAGCCCGCTCAAGGCGGAGTG 566
QY 544 GAGACCAACACACCTCCAAACAAGCAACAAGTACCGCGCCAGCAGCTACCTGAGC 603
Db 567 GAGACCAACACACCTCCAAACAAGCAACAAGTACCGCGCCAGCAGCTACCTGAGC 626
QY 604 CTGACGCTGAGCAGTGGAGTCCCAACAAGCTACAGTGCAGGTCAGCGCATGAAGGG 663
Db 627 CTGACGCTGAGCAGTGGAGTCCCAACAAGCTACAGTGCAGGTCAGCGCATGAAGGG 686
QY 664 AGCACGCTGAGAGCAGTGGCGCTTACAGATGTTTCAT 703
Db 687 AGCACGCTGAGAGCAGTGGCGCTTACAGATGTTTCAT 726

RESULT 9

US-09-152-060-29
; Sequence 29, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 29

; LENGTH: 879

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-29

Query Match 61.6%; Score 434; DB 4; Length 879;
Best Local Similarity 81.1%; Pred No. 4.1e-111; Indels 1;

Matches 519; Conservative 0; Mismatches 115; Gaps 6; Gaps 1;

QY 70 CTGACTCAGCCACCTCGGTGTCTGCTCCAGGACAGAGCCAGGATCACTGTGGG 129

Db 79 CTGACTCAGCCACCTCGGTGTCTGCTCCAGGACAGAGCCAGGATCACTGTGGG 138

QY 130 GGAGCAACAGTAGAATG-----AATATGTCCTGTTACAGCAGAGCAGCGCGG 183

Db 139 GGGAAACAACAATGTTGGCGACCAAGGAGCAGCTTGGCTGCAGCAGCAGCCAGGCCAC 198

QY 184 GCCCTTATCTGTCATCTATGATGATAGTACCGGCCCTCAGGGATCCCTGAGCGATTTC 243

Db 199 CCTCCAAACTCTGTCTTACAGGAATAATAACCGGCCCTCAGGGATCTCAGAGATTTC 258

QY 244 TCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCAGGCGCGGGAT 303

Db 259 TCTGCATCCAGTCTCAGGACCCACATCTCCCTGACCAATTAAGTCTCAGCTGAGGAC 318

QY 304 GAGGCTGACTATTACTGTCAGGTCGAGGACAGGGCTAGTGATCATCCGGTCTTTCGAGGA 363

Db 319 GAGGCTGACTATTACTGTCGAGCAGATATGACAGCAGCCTCGCAGTTTGGATGTTTCGCGGA 378

QY 364 GGGACCGGGTCAGCGTCTAGTGCAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCG 423

Db 379 GGGACCAAGCTGACCGTCTAGTGCAGCCCAAGGCTGCCCGCTCGGTCACTCTGTTCCCA 438

QY 424 CCTCTCTGAGGAGCTTCAAGCCAAAGGCGACACTGGTGTCTCATAGTGACTTC 483

Db 439 CCTCTCTGAGGAGCTTCAAGCCAAAGGCGACACTGGTGTCTCATAGTGACTTC 498

QY 484 TACCGGGAGCGTGCAGTGCCTGGAAGGAGATAGCAGCCCGCTCAAGGCGGAGTG 543

Db 499 TACCGGGAGCGTGCAGTGCCTGGAAGGAGATAGCAGCCCGCTCAAGGCGGAGTG 558

QY 544 GAGACCAACACACCTCCAAACAAGCAACAAGTACCGCGCCAGCAGCTACCTGAGC 603

Db 559 GAGACCAACACACCTCCAAACAAGCAACAAGTACCGCGCCAGCAGCTACCTGAGC 618

QY 604 CTGACGCTGAGCAGTGGAGTCCCAACAAGCTACAGTGCAGGTCAGCATGAAGGG 663

Db 619 CTGACGCTGAGCAGTGGAGTCCCAACAAGCTACAGTGCAGGTCAGCATGAAGGG 678

QY 664 AGCACGCTGAGAGCAGTGGCGCTTACAGATGTTTCAT 703

Db 679 AGCACGCTGAGAGCAGTGGCGCTTACAGATGTTTCAT 718

RESULT 10

US-09-152-060-46/c
; Sequence 46, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100

Db 185 TGCGTTGAGCTCTGGCTCAGTCTCTACTAGTAACACCCAGCTGGTACAGCAGACCCC 244
Qy 177 AGCGCGGCGCCCTATCTACTGCTCATCTATGATGATGACCGGCGCTCAGGGATCCCTGA 236
Db 245 AGCGAGGCTCCACGCGCTCATATACGCAAGTGTCTCTTCTGGATCCCTGA 304
Qy 237 GCGATTCTCTGGCTCCAAATCAGGGAACACCGCAACCTGACCATCAACGCGGTGAGGC 296
Db 305 TCCTCTCTCTGGCTCCATCTCTGGGAACAAAGCGGCTCACCATCAGCGGCGCCAGGC 364
Qy 297 CGGGGATGAGCTGACTATTACTGTCAGGTGGGAGGAGGCTAGTATCATCCGCTCT 356
Db 365 AGATGATGATCTGATTAATTATGT---GTCTATATAGGCGTAGTGGTCTTGGGTGT 421
Qy 357 CGGAGGAGGACCGCGGTGACCGCTCTAGGTACGCAAGGCTGCCCCCTCGGTCTACTCT 416
Db 422 CGCGGAGGACCAAGCTGTCCGTCTAGTCTAGCTAGCCCAAGGCTGCCCCCTCGGTCTACTCT 481
Qy 417 GTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAAAGGCCACACTGTGTGTCTCTAAG 476
Db 482 GTTCCCAACCTCTCTGAGGAGCTTCAAGCAACAAAGGCCACACTGTGTGTCTCTAAG 541
Qy 477 TGACTTCTACCGGAGCGGTGACAGTGGCGCTGGAAGGAGATAGCAGCCCGCTCAGGC 536
Db 542 TGACTTCTACCGGAGCGGTGACAGTGGCGCTGGAAGGAGATAGCAGCCCGCTCAGGC 601
Qy 537 GCGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTA 596
Db 602 GCGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTA 661
Qy 597 CTTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCGAGTCAAGCA 656
Db 662 CTTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCGAGTCAAGCA 721
Qy 657 TGAAGGAGCAGCTGAGAGAGCAGTGGCGCCCTCAGCAATGTTAT 703
Db 722 TGAAGGAGCAGCTGAGAGAGCAGTGGCGCCCTCAGCAATGTTAT 768

RESULT 12

US-08-793-450-5
; Sequence 5, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABIRI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 716 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..716
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..57
; NAME/KEY: mat_peptide
; LOCATION: 58..716
; OTHER INFORMATION: /product= "IMMUNOGLOBIN, LIGHT"
; OTHER INFORMATION: CHAIN"
; US-08-793-450-5

Query Match 57.8%; Score 407.4; DB 4; Length 716;

Best Local Similarity 78.0%; Pred. No. 8,9e-104;

Matches 536; Conservative 0; Mismatches 106; Indels 45; Gaps 2;

Qy 47 CAGGTGCGAGTGTGCTATGAATGACTCAGCCACCTCGGTGTGAGTGTCTCCAGGAC 106

Db 44 CAGGTGTCCACTCCGACATCGAGTCACTCAGGACCTGTGTGTCTGTGGCTTGGGAC 103

Qy 107 AGACGCCAGGATCACTGTGGGGAGACAAAGTAGAATATGTCCACTGTGATC 166

Db 104 AGACAGTCAAGATCACTGCCAAGGAGACAGCTCAGAACCTATTATGCAAGTGTGATC 163

Qy 167 AGCAGAAAGCAGCGCGGCGCTTATCTGTCTATCTATGATGATGATGACCGGCTCAG 226

Db 164 AGCAGAAAGCAGGACAGGACCTGTATCTATGTTGTTAAACAAACCGGCTCAG 223

Qy 227 GGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGGAAACACCGCCACCTGACCATCAAG 286

Db 224 GGATCCAGACCGATTCTCTGGCTCCAGCTCAGGAAACACAGCTTCTTTGACCATCACTG 283

Qy 287 GGGTCGAGGCCCGGGATGAGGCTGACTATTACTGTCTAGGTGTGGGACAGGGCTAGTATC 346

Db 284 GGGCTCAGCGGGAAGATAGGCTGACTATTCTGTAA-----CAGCGGTG 328

Qy 347 ATCCGGTCTTCGAGGAGGAGACCGGGTGAACCGGTCTCTAGGTGACGCCAAGGCTGCCCT 406

Db 329 GGAAGGTGTTCGCGGAGGAGCAAGCTGACCGTCTCTAGGTGACGCCAAGGCTGCCCT 388

Qy 407 CGGTCACTCTGTTCGCGCTCC-----TCTGAGG 436

Db 389 CGGTCACTCTGTTCGCGCTCCCTCCTCAGGAGCTTCAAGCAACAAAGGCCACACTCGAGG 448

Qy 437 AGCTTCAAGCCAAACAGGCCACACTGGTGTGTCTATAGTACTTCTACCCGGGAGCCG 496

Db 449 AGCTTCAAGCCAAACAGGCCACACTAGTGTGTCTGATCAGTACTTCTACCCGGGAGCTG 508

Qy 497 TGACAGTGGCTTGAAGGAGGATAGCAGCCCGTCAAGCGGAGTGGAGACCAACACAC 556

Db 509 TGACATTGGCTTGAAGGAGGATGGCAGGCCCGTCAAGCGGAGTGGAGACCAACAAAC 568

Qy 557 CCTCCAAACAAAGCAACAAAGTACCGGCCACAGCTACTCTGAGCCTTGAGCCTTGAGC 616

Db 569 CCTCCAAACAGAGCAACAAAGTACCGGCCACAGCTACTCTGAGCCTTGAGCCTTGAGC 628

Qy 617 AGTGGAGTCCCAACAGAGCTACAGCTGCGAGGTACGATGAGGAGGACCGTGGAGA 676

Db 629 AGTGGAGTCCCAACAGAGCTACAGCTGCGAGGTACGATGAGGAGGAGCTGACAGAGA 688

QY 677 AGACAGTGGCCCTACAGATGTTTCAT 703
|||||
Db 689 AGACGGTGGCCCTCGCAGATGTTTCAT 715

RESULT 13

US-09-404-879A-268/c
; Sequence 268, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404, 879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 268
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(584)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-268

Query Match 43.5%; Score 306.6; DB 4; Length 584;
Best Local Similarity 85.0%; Pred. No. 6.8e-76;
Matches 367; Conservative 0; Mismatches 57; Indels 8; Gaps 2;
QY 215 ACCGGCCCTCAGGATTCCTGAGCGATTCTCTGGCTCCAAATCAGGG-----AACACCGC 269
Db 449 AGCGGCCCTCAGGGGTCCCTGATCGCTTNTCTGGCTTCCAAGTCTTGGCAAAACACGGGCC 390
QY 270 CACCCTGACCATCAACGGGGTCGAGCGGGGATGAGGCTGACTATTACTTGTGACGGTGTG 329
Db 389 TCCTTTGACNGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTACTTGTGACGCTCATA 330
QY 330 GGACAGGGCTAGTGATCATCCGGTCTTCGGAGAGGAGACCCGGGTGACCCCTCTAGGTCA 389
Db 329 TGCAGGCAACA---ACAATTGGGTGTTTCGGCGAGGGACCAAGCTGACCGTCTCTAGGTCA 273
QY 390 GCCCAAGGCTGCCCGCTCGGTCACTCTGTTTCCCGCCCTCTCTGTGAGGAGCTTCAAGCCAA 449
Db 272 GCCCAAGGCTGCCCGCTCGGTCACTCTGTTTCCCAACCCCTCTCTGAGGAGCTTCAAGCCAA 213
QY 450 CAAGGCCACACTGGTGTCTCATATAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTG 509
Db 212 CAAGGCCACACTGGTGTCTCATATAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTG 153
QY 510 GAAGGCAGATAGCAGCCCGCTCAAGCGGGGAGTGGAGACCAACACACCCCTCCAAACAAAG 569
Db 152 GAAGGCAGATAGCAGCCCGCTCAAGCGGGGAGTGGAGACCAACACACCCCTCCAAACAAAG 93
QY 570 CAACAACAAGTACCGGCCACGAGCTACTTGAAGCTGAGCCCTGAGCAGTGGGAAGTCCCA 629
Db 92 CAACAACAAGTACCGGCCACGAGCTACTTGAAGCTGAGCCCTGAGCAGTGGGAAGTCCCA 33
QY 630 CAGAAGCTACAG 641
Db 32 CAGAAGCTACAG 21

RESULT 14

US-08-991-789A-241/c
; Sequence 241, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:

APPLICANT: Fridakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-08-991-789A-241

Query Match 38.8%; Score 273.2; DB 4; Length 771;
Best Local Similarity 79.2%; Pred. No. 1.3e-66;
Matches 336; Conservative 0; Mismatches 85; Indels 3; Gaps 1;
QY 131 GAGCAACAGTAGAATGAATATGTCCTGCTACAGCAGAGCAGCGCGGCCCTTA 190
Db 430 GTGACGTTGGTGTATATATATGTTCTNTGTGTACCAACAGCACCAGCAAGCCCA 371
QY 191 TACTGTCATCTATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT 250
Db 370 AATTCATGATTATGAGGTCGGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCT 311
QY 251 CCAATTCAGGAAACACCGCCACCTGACCATCAACAGGGGTGAGGCGCGGGATGAGGCTG 310
Db 310 CCAAGTNTGGCAACACCGCCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGCTG 251
QY 311 ACTATTACTGTGAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGAGGAGGAGCC 370
Db 250 ATTATTACTG---CAGCTCATATACAAGCAGCAGCACTCTCGTGTGTTGGCGGAGGACCA 194
QY 371 GGGTGACCGCTCTAGGTGACGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCGCCCTCTCT 430
Db 193 AGCTGACCGCTCTAGGTGACGCCCAAGGCTGCCCTCGGTCACTCTGTTCGCGCCCTCTCT 134
QY 431 CTGAGAGCTTCAAGCCAAAGGGCCACACTGGTGTGTCTCATAGTGACTTCTACCCCG 490
Db 133 CTGAGAGCTTCAAGCCAAAGGGCCACACTGGTGTGTCTCATAGTGACTTCTACCCCG 74
QY 491 GAGCGCTGACAGTGGCTTGGAAAGGAGATAGCAGCCCGCTCAAGCGCGGAGTGGAGACCA 550
Db 73 GAGCGCTGACAGTGGCTTGGAAAGGAGATAGCAGCCCGCTCAAGCGCGGAGTGGAGACCA 14

QY 551 CCAC 554
Db 13 CTAC 10

RESULT 15

US-09-062-451-241/C
; Sequence 241, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,451
; FILING DATE: 04-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.419C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 241:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-062-451-241

Query Match 38.8%; Score 273.2; DB 4; Length 771;
Best Local Similarity 79.2%; Pred. No. 1.3e-66;
Matches 336; Conservative 0; Mismatches 85; Indels 3; Gaps 1;
QY 131 GAGACAACAGTAGAATATGTCTCAGTGTACAGCAGAGCCAGCGCGGCCCTTA 190
Db 430 GTGACGTTGGTGGTTATAATAATCTCTCTGTGTACCAAGCAGCCAGGCAAGCCCA 371
QY 191 TACTGTGTCATGATGATGACGGCCCTCAGGATCCCTGAGCGATTCTCTGGCT 250
Db 370 AATTCATGATTTATGAGGTCGGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCT 311
QY 251 CCAATCAGGGAAACCGCCACCCCTGACCATCAACGGGGTCAGGCGGGGATGAGGCTG 310
Db 310 CCAAGTNTGGCAACAGGCTCTCCTGACCATCTCTGGGCTCCAGGCTGAGGAGGCTG 251
QY 311 ACTATTACTGTCTAGGTGTGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGAGGACCC 370
Db 250 ATTATTACTG---CAGCTCATATACAAGCAGCAGCACTCTCGTGTGTTGGCGGAGGACCA 194
QY 371 GGTGACCGCTCTAGGTACGCCCAAGCTGCCCCCTCGGTCACTCTGTTCGCCGCCCTCCT 430
Db 193 AGCTGACCGTCTAGGTACGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCGCCGCCCTCCT 134

QY 431 CTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCATAAGTACTTCTACCCGG 490
Db 133 CTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTGTCTCATAAGTACTTCTACCCGG 74
QY 491 GAGCCGTGACAGTGGCTGGAAGGCGAGATAGCAGCCCGTCAAGGCGGAGTGGAGACCA 550
Db 73 GAGCCGTGACAGTGGCTGGAAGGCGAGATAGCAGCCCGTCAAGGCGGAGTGGAGACCA 14
QY 551 CCAC 554
Db 13 CTAC 10

Search completed: June 3, 2003, 19:32:27
Job time : 44.2104 secs

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